

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:41:36 ; Search time 39 Seconds
(without alignments)
186.075 Million cell updates/sec

Title: US-10-612-885a-1
Perfect score: 117
Sequence: 1 ORVEILEGRTECVLSNLRGRTRY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP archaea:*
2: SP bacteria:*
3: SP fungi:*
4: SP human:*
5: SP invertebrate:*
6: SP mammal:*
7: SP mhc:*
8: SP organelle:*
9: SP phage:*
10: SP plant:*
11: SP rodent:*
12: SP virus:*
13: SP vertebrate:*
14: SP unclassified:*
15: SP virus:*
16: SP bacteriophage:*
17: SP archaea:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	109	93.2	316	11	Q35545
2	107	91.5	509	6	Q9MY29
3	104	88.9	229	6	Q28206
4	104	88.9	229	6	Q27950
5	104	88.9	387	6	Q95N13
6	104	88.9	418	6	Q95N14
7	56	47.9	176	17	Q8TYF5
8	52	44.4	1028	4	Q9UQ52
9	49	41.9	826	2	Q9AKX8
10	48	41.9	1028	11	P97528
11	48	41.0	428	10	Q9LPY7
12	48	41.0	1028	11	Q9UW88
13	48	41.0	1028	11	Q8C6X1
14	47	40.2	539	10	Q94LS6
15	47	40.2	539	10	Q7XDN4
16	47	40.2	640	10	Q9ASX3

17	47	40.2	644	10	Q8LDV1	Q8LDV1 arabidopsis
18	47	40.2	644	10	Q9FNK3	Q9FNK3 arabidopsis
19	47	40.2	1226	16	Q7UJ12	Q7UJ12 rhodospirillum rubrum
20	47	40.2	1873	10	Q9RC11	Q9RC11 arabidopsis
21	46	39.3	288	12	Q98214	Q98214 molluscum c
22	46	39.3	637	5	Q86G09	Q86G09 dictyostelium
23	46	39.3	700	11	Q9CXF5	Q9CXF5 mus musculus
24	46	39.3	700	11	Q8C0B3	Q8C0B3 mus musculus
25	46	39.3	781	15	Q82857	Q82857 jembrana di
26	46	39.3	1283	5	Q8TA82	Q8TA82 caenorhabdi
27	45.5	38.9	95	3	Q8TR83	Q8TR83 agrocycbe ae
28	45	38.5	76	7	Q30734	Q30734 macaca fusc
29	45	38.5	76	7	Q30567	Q30567 macaca fusc
30	45	38.5	81	7	Q30747	Q30747 macaca fusc
31	45	38.5	316	16	Q912J3	Q912J3 pseudomonas
32	45	38.5	446	10	Q94CT7	Q94CT7 oryza sativ
33	45	38.5	479	5	Q9U7P5	Q9U7P5 eufoillia
34	45	38.5	567	5	Q95R48	Q95R48 drosophila
35	45	38.5	567	5	Q9VCA3	Q9VCA3 drosophila
36	45	38.5	773	16	Q8A0C0	Q8A0C0 bacteroides
37	45	38.5	968	5	Q7YZ47	Q7YZ47 cryptospori
38	45	38.5	1056	12	Q57161	Q57161 spinach lat
39	44.5	38.0	691	5	Q9VW11	Q9VW11 drosophila
40	44.5	38.0	693	5	Q96680	Q96680 drosophila
41	44.5	38.0	810	10	Q92W13	Q92W13 cucurbita m
42	44	37.6	47	16	Q8XFL2	Q8XFL2 salmone
43	44	37.6	195	16	Q8Z0G3	Q8Z0G3 anabaena sp
44	44	37.6	606	5	Q9WRP6	Q9WRP6 drosophila
45	44	37.6	2023	12	Q91632	Q91632 cherry gree

ALIGNMENTS

RESULT 1	ID	SEQUENCE	PRELIMINARY	PRT	316 AA.
AC	Q35545				
DT	01-JAN-1998	(TREMBLER, 05, Created)			
DT	01-JAN-1998	(TREMBLER, 05, Last sequence update)			
DT	01-OCT-2003	(TREMBLER, 25, Last annotation update)			
DE	Intron 5-Inserted form of erythropoietin receptor precursor.				
OS	Rattus norvegicus (Rat).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.				
OX	NCBI_TaxID=10116;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=98296111; PubMed=9630610;				
RA	Yamaji R., Murakami C., Takenoshita M., Tsuyama S., Inui H.,				
RA	Miyatake K., Nakano Y.,				
RT	"The Intron 5-Inserted form of rat erythropoietin receptor is				
RT	expressed as a membrane-bound form."				
RL	Biochim. Biophys. Acta 1403:169-178(1998).				
DR	EMBL: D83509; BAA22373.1; -				
DR	HGSP: P19235; IEBA.				
DR	GO: GO:0016020; C:membrane; IEA.				
DR	GO: GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.				
DR	GO: GO:0004872; F:receptor activity; IEA.				
DR	InterPro: IPR002996; CRIA.				
DR	InterPro: IPR003961; FN.III.				
DR	InterPro: IPR008957; FN.III-like.				
DR	InterPro: IPR003528; Hematopoietin_L_F1.				
DR	Pfam: PF00041; fn3; 1.				
DR	SMART: SM00060; FN3; 1.				
DR	PROSITE: PS01352; HEMATOPOI_REC_L_F1; 1.				
KW	Receptor; signal.				
FT	SIGNAL	1	24	POTENTIAL.	
FT	CHAIN	25	316	POTENTIAL.	
SQ	SEQUENCE	316 AA; 34220 MW; 05C44BF516C180B CRC64;			

Query Match 93.2%; Score 109; DB 11; Length 316;
Best Local Similarity 91.3%; Pred. No. 6.8e-10;

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Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QRVELIGRTECVLSNLRGTRY 23
Db 193 QRVELIGRTECVLSNLRGTRY 215

RESULT 2
Q9MWZ9 PRELIMINARY; PRT; 509 AA.
AC Q9MWZ9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Erythropoietin receptor.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
RN [1] NCBI_TaxID=9823;
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Pearson F.L., Smith T.P.L., Sonstegard T.S., Klemcke H.G.,
RA Christenson R.K., Vallet J.L.;
RT "Porcine Erythropoietin Receptor: Molecular Cloning and Expression in
RT Embryonic and Fetal Liver.";
RT Domest. Anim. Endocrinol. 0:0-0(2000).
RL EMBL; AF274305; AAF77065.1; -.
DR HSSP; P19235; IEBA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtopoptn_L_Fl.
DR InterPro; IPR000572; Oxidored_mol_yb.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_Fl; 1.
DR PROSITE; PS00559; MOLYHDOPTERIN_EUK; 1.
KM Receptor.
SQ SEQUENCE 509 AA; 55183 MW; 35B565D07C6BDB8A CRC64;

Query Match 91.5%; Score 107; DB 6; Length 509;
Best Local Similarity 91.3%; Pred. No. 2.5e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QRVELIGRTECVLSNLRGTRY 23
Db 195 QRVELIGRTECVLSNLRGTRY 217

RESULT 3
Q28206 PRELIMINARY; PRT; 229 AA.
AC Q28206;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Erythropoietin receptor (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1] NCBI_TaxID=9913;
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Suliman H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.

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DR EMBL; U61399; AAB03871.1; -.
DR HSSP; P19235; IEBA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtopoptn_L_Fl.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_Fl; 1.
KM Receptor.
FT NON_TER 1 1
FT NON_TER 229 229
SQ SEQUENCE 229 AA; 25170 MW; EDFAA6F110D992E8 CRC64;

Query Match 88.9%; Score 104; DB 6; Length 229;
Best Local Similarity 87.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QRVELIGRTECVLSNLRGTRY 23
Db 136 QRVELIGRTECVLSNLRGTRY 158

RESULT 4
Q27950 PRELIMINARY; PRT; 229 AA.
AC Q27950;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Erythropoietin receptor (Fragment).
OS Bos indicus (Zebu).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1] NCBI_TaxID=9915;
RP SEQUENCE FROM N.A.
RC TISSUE=Bone marrow;
RA Suliman H.B., Feldman B.F., Majiwa P.A.O., Logan-Henfrey L.L.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U61398; AAB03870.1; -.
DR HSSP; P19235; IEBA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003528; Hemtopoptn_L_Fl.
DR Pfam; PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_Fl; 1.
KM Receptor.
FT NON_TER 1 1
FT NON_TER 229 229
SQ SEQUENCE 229 AA; 25196 MW; F6E01C4AB07893E8 CRC64;

Query Match 88.9%; Score 104; DB 6; Length 229;
Best Local Similarity 87.0%; Pred. No. 3.3e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 QRVELIGRTECVLSNLRGTRY 23
Db 136 QRVELIGRTECVLSNLRGTRY 158

RESULT 5
Q95N13

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ID Q95N13 PRELIMINARY; PRT; 387 AA.
AC Q95N13;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Erythropoietin receptor (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
OX
RN
RP SEQUENCE FROM N.A.
RA David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.;
RT "Quantitation of the mRNA levels of Epo and Epor in various tissues in
the ovine fetus.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029232; AAK8737.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hemtopoptn_L_Fl.
DR Pfam; PF00041; fn3; 1.
DR SMART; SMO0060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_Fl; 1.
KW Receptor.
FT NON_TER 1 387
SQ SEQUENCE 387 AA; 42039 MW; 0D1E6173C432EBC6 CRC64;

Query Match 88.9%; Score 104; DB 6; Length 387;
Best Local Similarity 87.0%; Pred. No. 5.9e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QRVETLGRTECVSLNLRGRTY 23
Db 130 QRVETLGRTECVSLNLRGRTY 152

RESULT 6
Q95N14 PRELIMINARY; PRT; 418 AA.
AC Q95N14;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Erythropoietin receptor (Fragment).
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
NCBI_TaxID=9940;
OX
RN
RP SEQUENCE FROM N.A.
RA David B., Lim G.B., Moritz K.M., Koukoulas I., Wintour M.;
RT "Quantitation of the mRNA levels of Epo and Epor in various tissues in
the ovine fetus.";
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY029231; AAK38170.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004896; F:hematopoietin/interferon-class (D200-domain. . .; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003528; Hemtopoptn_L_Fl.
DR Pfam; PF00041; fn3; 1.
DR SMART; SMO0060; FN3; 1.
DR PROSITE; PS01352; HEMATOPO_REC_L_Fl; 1.
KW Receptor.
FT NON_TER 1 418
SQ SEQUENCE 418 AA; 45282 MW; BB742EBEA034503C CRC64;
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SQ SEQUENCE 418 AA; 45282 MW; BB742EBEA034503C CRC64;
Query Match 88.9%; Score 104; DB 6; Length 418;
Best Local Similarity 87.0%; Pred. No. 6.4e-09;
Matches 20; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 QRVETLGRTECVSLNLRGRTY 23
Db 130 QRVETLGRTECVSLNLRGRTY 152

RESULT 7
Q9U052 PRELIMINARY; PRT; 176 AA.
AC Q9U052;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Uncharacterized protein.
OS Methanopyrus kandleri.
OC Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae;
OC Methanopyrus.
NCBI_TaxID=2320;
OX
RN
RP SEQUENCE FROM N.A.
RA STRAIN=AV19 / DSM 6324 / JCM 9639;
RX MEDLINE=21927647; PubMed=11930014;
RA Slesarev A.I., Mezheva K.V., Makarova K.S., Polushin N.N.,
RA Shcherbina O.V., Shakhova V.V., Belova G.I., Aravind L.,
RA Natsale D.A., Rogozin I.B., Tatusov R.L., Wolf Y.I., Stetter K.O.,
RA Malyskh A.G., Koonin E.V., Kozhavkin S.A.;
RT "The complete genome of hyperthermophile Methanopyrus kandleri AV19
and monophyly of archaeal methanogens.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4644-4649(2002).
DR EMBL; AE010332; AM01560.1; -.
DR InterPro; IPR009003; Cys_Ser_trypsin.
KW Complete proteome.
SQ SEQUENCE 176 AA; 19285 MW; 81E181C7BF3BDB8B CRC64;

Query Match 47.9%; Score 56; DB 17; Length 176;
Best Local Similarity 52.4%; Pred. No. 0.3;
Matches 11; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Oy 2 RVETLGRTECVSLNLRGRTY 22
Db 150 RMDVIBRTALRKLGRGR 170

RESULT 8
Q9U052 PRELIMINARY; PRT; 1028 AA.
AC Q9U052;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Neural adhesion molecule NB-3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NCBI_TaxID=9606;
OX
RN
RP SEQUENCE FROM N.A.
RA MEDLINE=9814618; PubMed=9486763;
RX Kamei Y., Tetsumi O., Takedani Y., Watanabe K.;
RT "CDNA cloning and chromosomal localization of neural adhesion
molecule, NB-3 in human.";
RL J. Neurosci. Res. 51:275-283(1998).
DR EMBL; AB003592; BA82612.1; -.
DR HSSP; P20241; ICFB.
DR Genew; HGNC:2176; CNTN6.
DR GO; GO:0007155; P:cell adhesion; TAS.
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DR GO:000717; P:central nervous system development; TAS.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_c2.
 DR Pfam: PF00041; fn3; 4.
 DR Pfam: PF00047; Ig; 6.
 DR SMART: SM00060; FN3; 3.
 DR SMART: SM00408; IGC2; 5.
 DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE: PS50835; IG_LIKE; 6.
 KW Immunoglobulin domain.
 SQ SEQUENCE 1028 AA; 113956 MW; 8B5A2BD2F2936A6 CRC64;

Query Match 44.4%; Score 52; DB 4; Length 1028;
 Best Local Similarity 71.4%; Pred. No. 9.9;
 Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 EGRTCYLSNLRGR 20
 Db 292 EGFYECLASNLNRGR 305

RESULT 9
 Q9AKX8 PRELIMINARY; PRT; 826 AA.
 AC Q9AKX8;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Hypothetical protein.
 OS Legionella pneumophila.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Legionellaceae; Legionella.
 NCBI_TaxID=446;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=serogroup 1;
 RX MEDLINE=21150471; PubMed=11251842;
 RA Iweneberg E., Mayer B., Daryab N., Kooistra O., Zaehner U.,
 Ronde M., Swanson J., Frosch M.;
 RT "Chromosomal insertion and excision of a 30 kb instable genetic
 element is responsible for phase variation of lipopolysaccharide and
 other virulence determinants in Legionella pneumophila.";
 RL Mol. Microbiol. 39:1259-1271(2001).
 DR EMBL: AJ277755; CAC33467.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 826 AA; 91581 MW; 4BD540C2665CFEF CRC64;

Query Match 41.9%; Score 49; DB 2; Length 826;
 Best Local Similarity 42.9%; Pred. No. 25;
 Matches 9; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QWVEILGRTECVLSNLRGR 21
 Db 782 RRAESNCRLETITSLKGRS 802

RESULT 10
 P97528 PRELIMINARY; PRT; 1028 AA.
 AC P97528;
 DT 01-MAY-1997 (TREMBlrel. 03, Created)
 DT 01-MAY-1997 (TREMBlrel. 03, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE NB-3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=Wistar; TISSUE=Brain;
 RX MEDLINE=97101230; PubMed=8945756;
 RA Ojawa J., Kaneko H., Masuda T., Nagata S., Hosoya H., Watanabe K.;
 RT "Novel neural adhesion molecules in the Contactin/F3 subgroup of the
 RT immunoglobulin superfamily: Isolation and characterization of cDNAs
 RT from rat brain.";
 RL Neurosci. Lett. 218:173-176(1996).
 DR EMBL: D87248; BA013320.1; -.
 DR GO:GO:0016020; C:membrane; IEA.
 DR GO:GO:0005524; F:ATP binding; IEA.
 DR GO:GO:0004009; F:ATP-binding cassette (ABC) transporter acti. .; IEA.
 DR GO:GO:0006810; P:transport; IEA.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR008957; FN_III-like.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003598; Ig_c2.
 DR Pfam: PF00041; fn3; 4.
 DR Pfam: PF00047; Ig; 6.
 DR SMART: SM00060; FN3; 4.
 DR SMART: SM00408; IGC2; 5.
 DR PROSITE: PS00211; ABC_TRANSPORTER_1; 1.
 DR PROSITE: PS50835; IG_LIKE; 6.
 KW Immunoglobulin domain.
 SQ SEQUENCE 1028 AA; 114065 MW; 47EPD8A370CF4923 CRC64;

Query Match 41.9%; Score 49; DB 11; Length 1028;
 Best Local Similarity 71.4%; Pred. No. 32;
 Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 EGRTCYLSNLRGR 20
 Db 292 EGFYECLASNLNRGR 305

RESULT 11
 Q9LPY7 PRELIMINARY; PRT; 428 AA.
 AC Q9LPY7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE T3J3J8.14.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shim P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S.,
 Kim C., Altfeld H., Bet O., Chin C., Chou J., Choi E., Conn L.,
 RA Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J.,
 RA Lenz C., Li J., Liu A., Liu K., Liu S., Mukharbek N., Nguyen M.,
 RA Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thavert A.,
 RA Tortini M., Vayberg M., Yu G., Federspiel N.A., Theologis A.,
 RA Ecker J.R.;
 RT "Genomic sequence for Arabidopsis thaliana BAC T3J3J8 from chromosome
 RT 1.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC011661; AAF16632.1; -.
 SQ SEQUENCE 428 AA; 48982 MW; 603F3FF2725622F9 CRC64;

Query Match 41.0%; Score 48; DB 10; Length 428;
 Best Local Similarity 45.5%; Pred. No. 18;
 Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

Qy 1 QWVEILGRTECVLSNLRGR 22
 Db 132 KRPQLENTTLCTLSRGR 153

RESULT 12

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09JMB8
ID 09JMB8 PRELIMINARY; PRT; 1028 AA.
AC 09JMB8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Neural recognition molecule NB-3.
GN CNTN6 OR MNB-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129SVJ; TISSUE=Brain;
RX MEDLINE=20183687; Pubmed=10717476;
RA Lee S., Takeda Y., Kawano H., Hosoya H., Nomoto M., Fujimoto D.,
RA Takahashi N., Watanabe K.;
RT "Expression and regulation of a gene encoding neural recognition
RT molecule NB-3 of the contactin/f3 subgroup in mouse brain.";
RL Gene 245:253-266(2000).
CC -1- SIMILARITY: CONTAINS 6 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
DR EMBL; AB032602; BAA92367.1; -.
DR HSSP; P20241; ICFB.
DR MGD; MGI:1858223; Cntn6.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 4.
DR Pfam; PF00047; Ig; 6.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00408; IgC2; 5.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00290; IG_MHC; 1.
KM Immunoglobulin domain.
SQ SEQUENCE 1028 AA; 113759 MW; AEECS9F86CA3978F CRC64;

Query Match 41.0%; Score 48; DB 11; Length 1028;
Best Local Similarity 64.3%; Pred. No. 47;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 EGRTECVLSNLGR 20
DB 292 EGFYECLAGNLGR 305

RESULT 13
ID 08C6X1 PRELIMINARY; PRT; 1028 AA.
AC 08C6X1;
DT 01-MAR-2003 (TREMBlrel. 23, Created)
DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Contactin 6.
GN CNTN6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Head;
RX MEDLINE=22354683; Pubmed=12466851;
RA The PANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
```

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RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK052872; BAC35227.1; -.
DR MGD; MGI:1858223; Cntn6.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004009; F:ATP-binding cassette (ABC) transporter acti. . .; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR008957; FN_III-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003598; Ig_c2.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 4.
DR Pfam; PF00047; Ig; 6.
DR SMART; SM00060; FN3; 4.
DR SMART; SM00409; Ig; 6.
DR SMART; SM00408; IgC2; 6.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.
DR PROSITE; PS50835; IG_LIKE; 6.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 1028 AA; 113761 MW; B23ED3008B1B101 CRC64;

Query Match 41.0%; Score 48; DB 11; Length 1028;
Best Local Similarity 64.3%; Pred. No. 47;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 7 EGRTECVLSNLGR 20
DB 292 EGFYECLAGNLGR 305

RESULT 14
ID 094LS6 PRELIMINARY; PRT; 539 AA.
AC 094LS6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DE 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxId=4530;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipondare;
RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance M., Shvartsbeyn M., Teltzin T.,
RA Riggs F., Heiao J., Zismann V., Blunt S., Pal G., Vanaken S.E.,
RA Utecherback T.R., Feldblyum T.V., Quackenbush J., Salberg S.L.,
RA White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSUTB0011A08 genomic sequence.";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC034258; AAK54287.1; -.
DR Gramene; Q94LS6; -.
KM Hypothetical protein.
SQ SEQUENCE 539 AA; 60201 MW; 8EBED40239310BC2 CRC64;

Query Match 40.2%; Score 47; DB 10; Length 539;
Best Local Similarity 56.2%; Pred. No. 34;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 EILEGTECVLSNLGR 19
DB 9 EVH8GTRSCVLSNLGR 24

RESULT 15
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07XDN4
ID 07XDN4 PRELIMINARY; PRT; 539 AA.
AC 07XDN4;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypoetical protein.
GN OSJNB0011A08.11.
OS Oryza sativa (Japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OK NCBI_taxid=39947;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA The Rice Chromosome 10 Sequencing Consortium;
RT "in-depth view of structure, activity, and evolution of rice
RL chromosome 10.";
RL Science 300:1566-1569(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RA Buell C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017102; AAP54107.1; -.
KM Hypoetical protein.
SQ SEQUENCE 539 AA; 60201 MW; 8EBED40239310BC2 CRC64;

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Query Match 40.2%; Score 47; DB 10; Length 539;
Best Local Similarity 56.2%; Pred. No. 34;
Matches 9; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

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QY 4 EILGRTCTVLSNLRG 19
   | : ||| | : ||
Db 9 EVHGGTRSCVILNVRG 24

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Search completed: May 6, 2004, 12:46:18
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:40:41 ; Search time 11 Seconds
(without alignments)
108.874 Million cell updates/sec

Title: US-10-612-885A-1
Perfect score: 117

Sequence: 1 QRVETLEGRECVLSNLRGRTRY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues
Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	100.0	508	EPOR_HUMAN	P19235 homo sapien
2	109	93.2	507	EPOR_MOUSE	P14753 mus musculu
3	109	93.2	507	EPOR_RAT	O07303 rattus norv
4	49	41.9	221	GIDB_BIRLO	Q06614 bifidobacte
5	49	41.9	473	KRM1_MOUSE	Q09n43 mus musculu
6	49	41.9	475	KRM1_HUMAN	Q06m48 homo sapien
7	48	41.0	312	PYRB_COREF	Q06f39 corynebacte
8	48	41.0	312	PYRB_COREG	Q09q38 corynebacte
9	47	40.2	956	TSP3_HUMAN	P49746 homo sapien
10	46	39.3	58	VSS9_ENTFA	Q03069 enterococcu
11	46	39.3	67	RS28_KL0LA	P33285 Kluyveromyc
12	46	39.3	67	RS28_KL0LA	P33286 Kluyveromyc
13	46	39.3	489	C128_MYCTU	Q05972 mycobacteri
14	46	39.3	697	AMS2_SCHPO	Q0ur4 schizosacch
15	46	39.3	1609	YL54_CABEL	P34434 caenorhabd
16	45.5	38.9	607	DB10_NICSY	P46942 nicotiana s
17	45	38.5	512	YR33_MYCTU	Q03228 mycobacteri
18	45	38.5	1036	AXOI_CHICK	P28685 gallus gall
19	44	37.6	473	KRM1_RAT	Q02464 rattus norv
20	43.5	37.2	269	FPFG_VIBPA	Q07f81 vibrio para
21	43	36.8	486	MURC_MOUSE	P43335 corynebacte
22	42.5	36.3	228	YAZ9_TREBA	O03992 treponema p
23	42.5	36.3	1912	PTPD_HUMAN	P23468 homo sapien
24	42.5	36.3	67	SHAS_YEAST	P13663 saccharomyc
25	42	35.9	365	DS28_YEAST	P13663 saccharomyc
26	42	35.9	482	THII_SALTI	Q028x1 salmonella
27	42	35.9	482	THII_SALTI	Q028x1 salmonella
28	42	35.9	482	THII_SALTI	Q028x1 salmonella
29	42	35.9	661	HCTC_PANIN	P00096 panulirus i
30	42	35.9	1020	CONT_MOUSE	P12960 mus musculu
31	42	35.9	1021	CONT_MOUSE	O63198 rattus norv
32	41.5	35.5	1897	PTPF_HUMAN	P10586 homo sapien
33	41	35.0	94	VE7_HPV37	Q08090 human papil

ALIGNMENTS

RESULT 1	EPOR_HUMAN	STANDARD;	PRT;	508 AA.
AC	P19235;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1990 (Rel. 16, Last sequence update)			
DT	15-MAR-2004 (Rel. 43, Last annotation update)			
DE	Erythropoietin receptor precursor (EPO-R).			
GN	EPOR.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=91372359; PubMed=1654273;			
RA	Etremman K., St John T.;			
RT	"The erythropoietin receptor gene: cloning and identification of			
RT	multiple transcripts in an erythroid cell line OCIM1."			
RL	Exp. Hematol. 19:973-977(1991).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90304340; PubMed=2163696;			
RA	Jones S.S., D'Andrea A.D., Haines L.L., Wong G.G.;			
RT	"Human erythropoietin receptor: cloning, expression, and biologic			
RT	characterization."			
RL	Blood 76:31-35(1990).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=92399733; PubMed=1668606;			
RA	Noguchi C.T., Bae K.S., Chin K., Wada Y., Schechter A.N.,			
RT	Hankins W.D.;			
RT	"Cloning of the human erythropoietin receptor gene."			
RL	Blood 78:2548-2556(1991).			
RN	[4]			
RP	SEQUENCE OF 1-96 FROM N.A.			
RC	TISSUE=Placenta;			
RX	MEDLINE=92399733; PubMed=1668607;			
RA	Mouche U., Tournamille C., Hattab C., Boffa G., Carttron J.-P.,			
RT	Chretien S.;			
RT	"Cloning of the gene encoding the human erythropoietin receptor."			
RL	Blood 78:2557-2563(1991).			
RN	[5]			
RP	SEQUENCE OF 1-17 FROM N.A.			
RX	MEDLINE=92147143; PubMed=1664413;			
RA	Penny L.A., Forget B.G.;			
RT	"Genomic organization of the human erythropoietin receptor gene."			
RL	Genomics 11:974-980(1991).			
RN	[6]			
RP	PHOSPHORYLATION AND INTERACTION WITH APS.			
RX	MEDLINE=9301417; PubMed=10374881;			
RA	Wakita T., Sasaki A., Mitsui K., Yokouchi M., Inoue A., Komiya S.,			
RA	Yoshimura A.;			
RT	"APS, an adaptor protein containing Pleckstrin homology (PH) and Src			
RT	homology-2 (SH2) domains inhibits the JAK-STAT pathway in			

34	41	35.0	200	1	RS4_THREVO	Q97b95 thermoplasma
35	41	35.0	292	1	GLIX_ECOLI	P77161 escherichia
36	41	35.0	346	1	XYNB_THRNE	O60041 thermotoga
37	41	35.0	413	1	PROA_CAUCR	Q9a2x6 caulobacter
38	41	35.0	416	1	Y997_ARCFU	O29265 archaeoglob
39	41	35.0	452	1	YHX7_YEAST	P38867 saccharomyc
40	41	35.0	479	1	PAX3_HUMAN	P23760 homo sapien
41	41	35.0	479	1	PAX3_MOUSE	P24610 mus musculu
42	41	35.0	520	1	PAX7_HUMAN	P23759 homo sapien
43	41	35.0	657	1	H57F_CABEL	P11411 caenorhabd1
44	41	35.0	833	1	DPO1_THEFI	O52225 thermus fil
45	41	35.0	833	1	PTIA_ECOLI	P32670 escherichia


```

RN [1]
RX MEDLINE=FROM N.A.
RX MEDLINE=69195238; PubMed=2539263;
RA D'Andrea A.D., Lodish H.F., Wong G.G.;
RT "Expression cloning of the murine erythropoietin receptor.";
RL Cell 57:277-285(1989).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Liver;
RX MEDLINE=91080149; PubMed=2175360;
RA Kuramochi S., Ikawa Y., Todokoro K.;
RT "Characterization of murine erythropoietin receptor genes.";
RL J. Mol. Biol. 216:567-575(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=92017832; PubMed=1656233;
RA Hirao M., Tojo A., Misawa Y., Morii H., Takaku F., Shibuya M.;
RT "Unregulated expression of the erythropoietin receptor gene caused by
RT insertion of spleen focus-forming virus long terminal repeat in a
RT murine erythroleukemia cell line.";
RL Mol. Cell. Biol. 11:5527-5533(1991).
RN [4]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE=99287158; PubMed=2162479;
RA Yousoufian H., Zon L.I., Orkin S.H., D'Andrea A.D., Lodish H.F.;
RT "Structure and transcription of the mouse erythropoietin receptor
RT gene.";
RL Mol. Cell. Biol. 10:3675-3682(1990).
RN [5]
RP SEQUENCE OF 1-24 FROM N.A.
RX MEDLINE=91201346; PubMed=1849897;
RA Lacombe C., Chretien S., Lemarchandel V., Mayeux P., Romeo P.H.,
RA Gieselsbrecht S., Cartron J.-P.;
RT "Spleen focus-forming virus long terminal repeat insertion1
RT activation of the murine erythropoietin receptor gene in the T3C1-2
RT friend leukemia cell line.";
RL J. Biol. Chem. 266:6952-6956(1991).
RN [6]
RP INTERACTION WITH APS.
RX MEDLINE=22510236; PubMed=1244928;
RA Wolberg P., Lemarsson J., Gottfridsson E., Yoshimura A.,
RA Romstrand L.;
RT "The adapter protein APS associates with the multifunctional docking
RT sites Tyr-568 and Tyr-936 in c-Klt.";
RL Biochem. J. 370:1033-1038(2003).
RN [7]
RP MUTAGENESIS.
RX MEDLINE=93180826; PubMed=8382775;
RA Miura O., Cleveland J.L., Ihle J.N.;
RT "Inactivation of erythropoietin receptor function by point mutations
RT in a region having homology with other cytokine receptors.";
RL Mol. Cell. Biol. 13:11788-11795(1993).
CC -1- FUNCTION: Receptor for erythropoietin. Mediates erythropoietin-
CC induced erythroid blast proliferation and differentiation. Upon EPO
CC stimulation, EPOR dimerizes triggering the JAK2/STAT5 signaling
CC cascade. Isoform 2 acts as a dominant-negative receptor for EPOR-
CC mediated signals.
CC -1- SUBUNIT: Interacts with APS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC Subfamily 1.
CC -1- SIMILARITY: Contains 1 fibronectin type III domain.
CC -----
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CC -----
DR EMBL, J04843; AAA37571.1; -.
DR EMBL, X53081; CAA37248.1; -.

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DR	EMBL; M38133; AAA37572.1; -;
DR	EMBL; M62360; AAA37582.1; -;
DR	EMBL; S59388; AAB20029.2; -;
DR	PIR; A4186; A4385.
DR	PIR; S14081; A14081.
DR	HSSP; P19235; IEBA.
DR	MED; MG1.95408; Eporf.
DR	InterPro; IPR002996; CRIA.
DR	InterPro; IPR008957; FN_III-like.
DR	InterPro; IPR003961; FN_III.
DR	InterPro; IPR00328; Hemtopopn_L_Ft.
DR	Pfam; PF00041; fn3; 1.
DR	PIRSF; PIRSF01959; Epo_receptor; 1.
DR	SMART; SM0060; FN3; 1.
DR	PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW	Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation.
FT	SIGNAL
FT	CHAIN
FT	DOMAIN
FT	TRANSMEM
FT	DOMAIN
FT	DOMAIN
FT	SITE
FT	DISULFD
FT	DISULFD
FT	MOD_RES
FT	CADBOHD
FT	CONFLICT
SO	SEQUENCE
Query Match	93.2%; Score 109; DB 1; Length 507;
Best Local Similarity	91.3%; Pred. No. 1,56-09;
Matches	21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Oy	1 ORVELLEGRTECVLSNLGRTRY 23
Db	193 QREVELEGRTICVLSNLGRGTRY 215
RESULT 3	
EPOP_RAT	
ID_EPOP_RAT	STANDARD; PRT; 507 AA.
AC	Q07303;
DT	01-FEB-1995 (Rel. 31, Created)
DT	01-FEB-1995 (Rel. 31, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Erythropoietin receptor precursor (EPO-R).
GN	EPOr.
OS	Rattus norvegicus (Rat).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX	NCB1_TaxID=10116;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEIDLIN=93266574; PubMed=7684373;
RA	Maesuda S., Nagao M., Takahata K., Konishi Y., Gallyas F.,
RA	Tabira T., Sasaki R.;
RT	"Functional erythropoietin receptor of the cells with neural
RT	characteristics. Comparison with receptor properties of erythroid
RT	cells.";
RL	J. Biol. Chem. 268:11208-11216(1993).
CC	-1- FUNCTION: Receptor for erythropoietin. Mediates erythropoietin-
CC	induced erythroblast proliferation and differentiation. Upon EPO
CC	stimulation, EPOr dimerizes triggering the JAK2/SYK5 signaling
CC	cascade. Isoform 2 acts as a dominant-negative receptor of EPOr-
CC	mediated signals.
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.
CC	-1- SIMILARITY: Belongs to the type I cytokine family of receptors.
CC	-1- SIMILARITY: Contains 1 fibronectin type III domain.
CC	-----
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CC -----
 DR EMBL, D13566; BAA02761.1; -.
 DR PIR, A46713; A46713.
 DR HSSP, P19235; IEBA.
 DR InterPro: IPRO02996; CRA.
 DR InterPro: IPRO08957; FN III-like.
 DR InterPro: IPRO03961; FN III.
 DR InterPro: IPRO03528; Hemtopoptn_L_F1.
 DR Pfam; PF00041; fn3; 1.
 DR PIRSF; PIRSF01959; EPO_receptor; 1.
 DR SMART; SMO0060; FN3; 1.
 DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
 DR Receptor; Transmembrane; Glycoprotein; Signal.
 KM SIGNAL 1 24
 FT CHAIN 1 25 507
 FT DOMAIN 25 249 ERYTHROPOIETIN RECEPTOR.
 FT TRANSMEM 250 272 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 273 507 POTENTIAL.
 FT DOMAIN 147 212 CYTOPLASMIC (POTENTIAL).
 FT DISULFID 52 62 FIBRONECTIN TYPE-III.
 FT DISULFID 90 106 BY SIMILARITY.
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 507 AA; 55499 MW; AC79AF22D06A7312 CRC64;

Query Match 93.2%; Score 109; DB 1; Length 507;
 Best Local Similarity 91.3%; Pred. No. 1.5e-09;
 Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QVVEILGRTECVSLNLRGRY 23
 Db 193 QVVEILGRTECVSLNLRGRTRY 215

RESULT 4
 GIDB_BIFLO STANDARD; PRT; 221 AA.
 AC Q86604;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Methyltransferase gldb (EC 2.1.1.-) (Glucose inhibited division
 DE protein B).
 GN GIDB OR BL0646.
 OS Bifidobacterium longum.
 OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
 CC Bifidobacteriaceae; Bifidobacterium.
 OX NCBI_TaxID=216816;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NCC 2705;
 RX MEDLINE=22294977; PubMed=12381787;
 RA Schell M.A., Karamitatzou M., Snel B., Vilanova D., Berger B.,
 RA Peesi G., Zwanhan M.-C., Desiere F., Bork P., Delley M.,
 RA Fridmore R.D., Arigoni F.;
 RT "The genome sequence of Bifidobacterium longum reflects its adaptation
 RT to the human gastrointestinal tract.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
 CC -1- FUNCTION: Probable S-adenosyl-L-methionine dependent
 CC methyltransferase specific for a sterol and/or lipid substrate (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the gldb family.

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CC -----
 DR EMBL; AE014686; AAN24468.1; -.
 DR HAMAP; MF 00074; -; 1.
 DR InterPro: IPRO03682; Gldb.
 DR Pfam; PF02527; Gldb; 1.
 DR ProDom; PD004441; Gldb; 1.
 DR TIGRFAMs; TIGR00138; gldb; 1.
 DR Transferase; Methyltransferase; Complete proteome.
 SQ SEQUENCE 221 AA; 24163 MW; FB131A5126368A05 CRC64;

Query Match 41.9%; Score 49; DB 1; Length 221;
 Best Local Similarity 45.0%; Pred. No. 1.8;
 Matches 9; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 QVVEILGRSDAVIQVYKR 139
 Db 120 QVVEILGRSDAVIQVYKR 139

RESULT 5
 KRM1_MOUSE STANDARD; PRT; 473 AA.
 AC Q99N43;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kremen protein 1 precursor (Kringel-containing protein marking the eye
 DE and the nose) (Dickkopf receptor).
 GN KREMENT OR KREMENT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., DEVELOPMENTAL STAGE, AND TISSUE SPECIFICITY.
 RC TISSUE=Brain, and Kidney;
 RX MEDLINE=21167372; PubMed=11267660;
 RA Nakamura T., Aoki S., Kitajima K., Takahashi T., Matsumoto K.,
 RA Nakamura T.;
 RT "Molecular cloning and characterization of Kremen, a novel
 RT kringel-containing transmembrane protein.";
 RL Biochim. Biophys. Acta 1518:63-72(2001).
 CC -1- FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf
 CC to block Wnt/beta-catenin signaling (by similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
 CC -1- TISSUE SPECIFICITY: In the adult, widely expressed with high
 CC levels in heart, lung, kidney, skeletal muscle and testis.
 CC -1- DEVELOPMENTAL STAGE: In the embryo, expression is first detected
 CC on day 9 and increases up to day 18. Lower levels are found in
 CC adult. At 9.5 dpc, expression is localised to the apical
 CC ectodermal ridge (AER) of the developing fore- and hindlimb buds,
 CC the telencephalon and the first brachial arch. At 10.5 dpc,
 CC expression is also observed in the myotome and in sensory tissues
 CC such as the nasal pit and optic vesicle.
 CC -1- SIMILARITY: Contains 1 CUB domain.
 CC -1- SIMILARITY: Contains 1 kringel domain.
 CC -1- SIMILARITY: Contains 1 MSC domain.

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CC -----
 DR EMBL; AB059617; BAB40968.1; -.
 DR HSSP; P00747; ICEA.
 DR MGD; MGI:193398; Kremen.
 DR GO; GO:0016021; C:integral to membrane; NMS.
 DR InterPro: IPRO00859; CUB.
 DR InterPro: IPRO00001; Kringel.

DR InterPro; IPR002889; WSC.
 DR Pfam; PF00431; CUB; 1.
 DR Pfam; PF00051; kringle_1.
 DR Pfam; PF01822; WSC; 1.
 DR PRINTS; PR00016; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00042; CUB; 1.
 DR SMART; SM00130; KR; 1.
 DR PROSITE; PS01180; CUB; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR Mut signaling pathway; Signal; Transmembrane; Kringle.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 473 KREMER PROTEIN 1.
 FT DOMAIN 21 392 EXTRACELLULAR (POTENTIAL).
 FT TRANSSEM 393 413 POTENTIAL.
 FT DOMAIN 414 473 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 120 210 WSC.
 FT DOMAIN 214 321 CUB.
 FT CARBOHYD 59 217 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 217 217 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 345 345 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 473 AA; 5176 MW; 586827788B3FDD1 CRC64;

Query Match 41.9%; Score 49; DB 1; Length 473;
 Best Local Similarity 55.0%; Pred. No. 4.1;
 Matches 11; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 VELLGRTCEVLNLRGRTR 22
 Db 268 VELLGRTCEVLNLRGRSR 287

RESULT 6
 KRM1_HUMAN STANDARD; PRT; 475 AA.
 ID Q96MU8; Q9BY70; Q9UGS5; Q9UGU1;
 AC 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Kremen protein 1 precursor (kringle-containing protein marking the eye and the nose) (Dickkopf receptor).
 DE KREMER1 OR KREMER.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Nakamura T., Nakamura T.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Iashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ichii S., Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Nagatsuma M., Murakawa K., Kanehori K., Takahashi-Fuji A., Oshima A., Sugiyama A., Murakami B., Suzuki Y., Sugano S., Nagahari K., Masuno Y., Nagai K., Iisoga T.;
 RA "MEDO human cDNA sequencing project";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20057165; PubMed=10591208;
 RA Dunham I., Hunt A.R., Collins J.E., Bruskewich R., Beare D.M., Clamp M., Smink L.J., Ainscough R., Almeida J.P., Babbage A.K., Baguley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P.,

RA Bird C.P., Blakey S.E., Bridgeman A.M., Buck D., Burgess J., Burrill W.D., Burton J., Carder C., Carter N.P., Chen Y., Clark G., Clegg S.M., Cobley V.E., Cole C.G., Collier R.E., Connor R., Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Dawson E., Dhani P.D., Dockree C., Dodsworth S.J., Durbin R.M., Ellington A.G., Evans K.L., Fey J.M., Fleming K., French L., Garner A.A., Hallbert J.G.R., Goward M.E., Graffham D.V., Griffiths M.N.D., Hall C., Hall R.E., Hall-Tamlyn G., Heathcote R.M., Ho S., Holmes S., Hunt S.E., Jones M.C., Kershaw J., Kimberley A.M., King J., Laird G.K., Langford C.F., Leversha M.A., Lloyd C., Lloyd D.M., Marlyn I.D., Mashreghi-Mohammadi M., Matthews L.H., McCann O.T., McClay J., McLaren S., McMuray A.A., Milne S.A., Mortimore B.J., Odell C.N., Pavitt R., Pearce A.V., Pearson D., Phillimore B.J.C.T., Phillips S.H., Plumb R.W., Ramsey H., Ramsey Y., Rogers L., Ross M.T., Scott C.E., Sehra H.K., Stuce C.D., Smalley S., Smith M.L., Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann R.M., Vaudin M., Wall M., Wallis J.M., Whiteley M.N., Willey D.L., Williams L., Williams S.A., Williamson H., Wilmer T.E., Wilming L., Wright C.L., Hubbard T., Bentley D.R., Beck S., Rogers J., Shimizu N., Manoshima S., Kawasaki K., Sasaki T., Asakawa S., Kudoh J., Shintani A., Shibuya K., Yoshizaki Y., Aoki N., Mitsuyama S., Roe B.A., Chen F., Chu L., Crabtree J., Deschamps S., Do A., Do T., Dorman A., Fang F., Fu Y., Hu P., Hua A., Kenton S., Lai H., Lao H.I., Lewis J., Lewis S., Lin S.-P., Loh P., Malaj E., Nguyen T., Pan H., Phan S., Qi S., Qian Y., Ray L., Ren O., Shaull S., Sloan D., Song L., Wang Q., Wang Y., Wang Z., White J., Willingham D., Wu H., Yao Z., Zhan M., Zhang G., Chisoe S., Murray J., Miller N., Mix P., Fulton R., Johnson D., Bemis G., Bentley D., Bradshaw H., Bourne S., Cordes M., Du Z., Fulton L., Goela D., Graves T., Hawkins J., Hinds K., Kemp K., Latreille P., Layman D., Ozerky P., Rolfing T., Schaefer P., Walker C., Wamley A., Wohlmann P., Pepin K., Nelson J., Korfi I., Bedell J.A., Hillier L.W., Mardis E., Waterston R., Wilson R., Emanuel B.S., Shaikh T., Kurahashi H., Saitta S., Budart M.L., McDermaid H.E., Johnson A., Wong A.C.C., Morrow B.E., Edelmann L., Kim U.J., Shizuya C., Simon M.I., Dumanski J.P., Peyrard M., Kedra D., Seroussi E., Franssen I., Tapia I., Bruder C.E., O'Brien K.P., Wilkinson P., Bodenteich A., Hartman K., Hu X., Khan A.S., Lane L., Tjilahun Y., Wright H.;
 RA "The DNA sequence of human chromosome 22";
 RL Nature 402:489-495(1999).
 CC - FUNCTION: Receptor for Dickkopf protein. Cooperates with Dickkopf to block Wnt/beta-catenin signaling (by similarity).
 CC - SUBCELLULAR LOCATION: Type I membrane protein (potential).
 CC - ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q96MU8-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q96MU8-2; Sequence=VSP_003900;
 CC Note=No experimental confirmation available;
 CC - SIMILARITY: Contains 1 CUB domain.
 CC - SIMILARITY: Contains 1 kringle domain.
 CC - SIMILARITY: Contains 1 WSC domain.
 CC -----
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 CC -----
 CC EMBL; AB059618; BAB40969.1; -;
 CC EMBL; AK056425; BAB71180.1; -;
 CC EMBL; Z95116; CAB62952.1; -;
 CC EMBL; AL021393; CAB62959.1; -;
 CC Genew; HGNC:17550; KREMER1.
 CC GO; GO:0016021; C:integral to membrane; ISS.
 CC GO; GO:0005624; C:membrane fraction; TAS.
 CC GO; GO:0007154; P:cell communication; TAS.
 CC InterPro; IPR000859; CUB.
 CC InterPro; IPR000001; Kringle.
 CC InterPro; IPR002889; WSC.

```
DR Pfam; PF00431; CUB; 1.
DR Pfam; PF00051; Kringles; 1.
DR Pfam; PF01822; WSC; 1.
DR PRINTS; PR00018; KRINGLE.
DR PRODOM; PD000395; Kringles; 1.
DR SMART; SM00042; CUB; 1.
DR SMART; SM00130; KR; 1.
DR PROSITE; PS01180; CUB; 1.
DR PROSITE; PS00021; KRINGLE 1; 1.
DR PROSITE; PS50070; KRINGLE 2; 1.
DR Wnt signaling pathway; Signal; Transmembrane; Kringles;
KW Alternative splicing.
FT SIGNAL 19
FT CHAIN 20 475
FT DOMAIN 21 394
FT TRANSMEM 395 415
FT DOMAIN 416 475
FT DOMAIN 33 116
FT DOMAIN 121 202
FT DOMAIN 216 323
FT CARBOHYD 47 47
FT CARBOHYD 61 61
FT CARBOHYD 219 219
FT CARBOHYD 295 295
FT CARBOHYD 335 335
FT CARBOHYD 347 347
FT VARSPIC 473 475
FT /FTID=VSP_003900.
FT MISSING (IN REF. 1).
FT I -> V (IN REF. 2).
SQ SEQUENCE 475 AA; 5198 MM; B7E86FD80F6A0A4 CRC64;

Query Match 41.9%; Score 49; DB 1; Length 475;
Best Local Similarity 50.0%; Pred. No. 4.1;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 VELEGRETCVLSNLGRGRT 22
DB 270 VELLGGITRVLAFHGRSR 289

RESULT 7
PYRB CORGF STANDARD; PRT; 312 AA.
AC Q8FTJ3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
transcarbamylase) (ATCase).
GN PYRB OR C61732.
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_Taxid=152794;
RX [1]
SEQUENCE FROM N.A.
STRAIN=YB-314 / AJ 12310 / DSM 44549 / JCM 11189;
RA Meshio Y., Nakamura Y., Kawarabayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsu K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
replacements responsible for the thermostability of Corynebacterium
efficiens."
RL Genome Res. 13:1572-1579(2003).
CC -1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate
+ N-carbamoyl-L-aspartate.
CC -1- PATHWAY: Pyrimidine biosynthesis; second step.
CC -1- SIMILARITY: Belongs to the ATCase/OTCase family.
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CC -----
DR EMBL; AP005219; BAC18542.1; ALT_INIT.
DR HAMAP; MF_00001; -; 1.
DR InterPro; IPR006130; Asp/Om Cofact.
DR InterPro; IPR002082; Asp cardmltransf.
DR InterPro; IPR006131; OTCase_O.
DR InterPro; IPR006132; OTCase_P.
DR Pfam; PF00185; OTCase; 1.
DR Pfam; PF02729; OTCase; N; 1.
DR PRINTS; PR00100; AOTCase.
DR TIGRfam; TIGR00670; asp_crb tr; 1.
DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; 1.
DR Pyrimidine biosynthesis; transferase; Complete proteome.
KW SEQUENCE 312 AA; 33706 MM; EEFA0AD98413D3B CRC64;

Query Match 41.0%; Score 48; DB 1; Length 312;
Best Local Similarity 61.1%; Pred. No. 3.7;
Matches 11; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 4 EILEGRETCVLSNLGRGRT 21
DB 27 EVLEGRHVKKLPTLRGRT 44

RESULT 8
PYRB CORGL STANDARD; PRT; 312 AA.
AC Q8N038;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Aspartate carbamoyltransferase (EC 2.1.3.2) (Aspartate
transcarbamylase) (ATCase).
GN PYRB OR C61612.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
NCBI_Taxid=1718;
RX [1]
SEQUENCE FROM N.A.
STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-aspartate = phosphate
+ N-carbamoyl-L-aspartate.
CC -1- PATHWAY: Pyrimidine biosynthesis; second step.
CC -1- SIMILARITY: Belongs to the ATCase/OTCase family.
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CC -----
DR EMBL; AP005279; BAB99005.1; -.
DR HAMAP; MF_00001; -; 1.
DR InterPro; IPR006130; Asp/Om Cofact.
DR InterPro; IPR002082; Asp cardmltransf.
DR InterPro; IPR006131; OTCase_O.
DR InterPro; IPR006132; OTCase_P.
DR Pfam; PF00185; OTCase; 1.
DR Pfam; PF02729; OTCase; N; 1.
DR PRINTS; PR00100; AOTCase.
DR TIGRfam; TIGR00670; asp_crb tr; 1.
```

QY	4	ELIEGRTECVLSNLRGT	21
Db	27	EVLEGRVKKLPTLRGRT	44
Query Match	41.0%	Score 48;	DB 1; Length 312;
Best Local Similarity	61.1%	Pred. No. 3.7;	
Matches	11;	Conservative 1;	Mismatches 6; Indels 0; Gaps
RESULT 9			
TS_P3_HUMAN		STANDARD;	PRT; 956 AA.
ID	P49746;	OBWV34;	
AC	01-OCT-1996	(Rel. 34, Created)	
DT	01-OCT-1996	(Rel. 34, Last sequence update)	
DT	10-OCT-2003	(Rel. 42, Last annotation update)	
DE	Thrombospondin 3 precursor.		
GN	THBS3 OR TSP3.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=Lung;		
RX	MEDLINE=96044440; PubMed=7558000;		
RA	Adolph K.W., Long G.L., Winfield S., Gims E.I., Bornstein P.,		
RT	Structure and organization of the human thrombospondin 3 gene		
RT	(THBS3)."		
RL	Genomics 27:329-336(1995).		
RN	[2]		
RP	SEQUENCE OF 1-736 FROM N.A.		
RX	MEDLINE=97474796; PubMed=9333372;		
RA	Winfield S.L., Tayebi N., Martin B.M., Gims E.I., Sidransky E.,		
RT	Identification of three additional genes contiguous to the		
RT	glucocerebrosidase locus on chromosome 1q21: implications for Gaucher		
RL	disease."		
RL	Genome Res. 7:1020-1026(1997).		
RN	[3]		
RP	SEQUENCE OF 365-956 FROM N.A.		
RC	TISSUE=Retina;		
RX	MEDLINE=22388257; PubMed=12477932;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,		
RA	Altschul S.F., Zeeberg K.B., Buetow K.H., Schaefer C.F., Bhat N.K.,		
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,		
RA	Dickenson L., Marusina K., Farmer A., Rubin G.M., Hong L.,		
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Rana S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullany S.J.,		
RA	Bohak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunnaratre P.H.,		
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahney J., Heltón E., Kettman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Bikesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywnski M.I., Skalska U., Smalins D.E.,		
RA	Schuerch A., Schein J.E., Jones S.J.M., Marra M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length		
RT	human and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:18699-18903(2002).		
CC	-1- FUNCTION: Adhesive glycoprotein that mediates cell-to-cell and		
CC	cell-to-matrix interactions. Can bind to fibrinogen, fibronectin,		
CC	laminin and type V collagen.		
CC	-1- SUBUNIT: Oligomer; disulfide-linked.		
CC	-1- SIMILARITY: Belongs to the thrombospondin family.		
CC	-1- SIMILARITY: Contains 4 EGF-like domains.		
CC	-1- SIMILARITY: Contains 7 TSP type-3 domains.		

CC	-1.	SIMILARITY:	Contains 1 TSP N-terminal (TSPN) domain.
CC	-----		
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CC	-----		
DR	EMBL; L38969;	AAC41762.1; -.	
DR	EMBL; A023256;	AAC51818.1; -.	
DR	EMBL; BC018786;	AAH18786.1; -.	
DR	PIR; A57121;	A57121.	
DR	HSSP; P35555;	IEMN.	
DR	GeneW; HGNC:11787;	TBBS3.	
DR	MIM; 188062;	-.	
DR	GO; GO:0005509;	P:calcium ion binding; TAS.	
DR	GO; GO:007160;	F:cell-matrix adhesion; TAS.	
DR	InterPro; IPR001881;	EGF_Ca.	
DR	InterPro; IPR006209;	EGF_like.	
DR	InterPro; IPR003367;	tsp_3.	
DR	InterPro; IPR008859;	TSPC.	
DR	InterPro; IPR003129;	TSPN.	
DR	Pfam; PF00008;	EGF; 1.	
DR	Pfam; PF02412;	tsp_3; 13.	
DR	Pfam; PF05735;	TSPC; 1.	
DR	Pfam; PF02210;	TSPN; 1.	
DR	SMART; SMO0210;	EGF_CA; 1.	
DR	SMART; SMO0222;	EGF_1; FALSE_NEG.	
DR	PROSITE; PS00022;	EGF_2; 1.	
DR	PROSITE; PS01186;	EGF_3; 3.	
DR	PROSITE; PS50026;	EGF_3; 3.	
DR	PROSITE; PS01187;	EGF_CA; 2.	
KM	Glycoprotein; Cell adhesion; Calcium-binding; Repeat;		
KM	EGF-like domain; Signal.		
FT	SIGNAL	1	POTENTIAL.
FT	CHAIN	22	THROMBOSPONDIN 3.
FT	DOMAIN	22	N-TERMINAL.
FT	DOMAIN	274	EGF-LIKE 1.
FT	DOMAIN	316	EGF-LIKE 2.
FT	DOMAIN	370	CALCIUM-BINDING (POTENTIAL).
FT	DOMAIN	413	EGF-LIKE 3.
FT	DOMAIN	414	EGF-LIKE 4.
FT	DOMAIN	488	TSP TYPE-3 1.
FT	DOMAIN	524	TSP TYPE-3 2.
FT	DOMAIN	547	TSP TYPE-3 3.
FT	DOMAIN	582	TSP TYPE-3 4.
FT	DOMAIN	583	TSP TYPE-3 5.
FT	DOMAIN	606	TSP TYPE-3 6.
FT	DOMAIN	644	TSP TYPE-3 7.
FT	DOMAIN	684	C-TERMINAL.
FT	DOMAIN	719	INTERCHAIN (PROBABLE).
FT	DISULFD	266	INTERCHAIN (PROBABLE).
FT	DISULFD	269	BY SIMILARITY.
FT	DISULFD	278	BY SIMILARITY.
FT	DISULFD	283	BY SIMILARITY.
FT	DISULFD	303	BY SIMILARITY.
FT	DISULFD	303	BY SIMILARITY.
FT	DISULFD	320	BY SIMILARITY.
FT	DISULFD	326	BY SIMILARITY.
FT	DISULFD	344	BY SIMILARITY.
FT	DISULFD	374	BY SIMILARITY.
FT	DISULFD	382	BY SIMILARITY.
FT	DISULFD	400	BY SIMILARITY.
FT	DISULFD	418	BY SIMILARITY.
FT	DISULFD	426	BY SIMILARITY.
FT	DISULFD	444	BY SIMILARITY.
FT	DISULFD	471	BY SIMILARITY.
FT	DISULFD	483	BY SIMILARITY.
FT	DISULFD	519	BY SIMILARITY.
FT	DISULFD	542	BY SIMILARITY.
FT	DISULFD	578	BY SIMILARITY.
FT	DISULFD	601	BY SIMILARITY.
FT	DISULFD	639	BY SIMILARITY.
FT	DISULFD	679	BY SIMILARITY.

```

FT DISULFID 715 936 BY SIMILARITY.
FT CARBOHYD 310 310 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 407 407 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 644 644 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 937 937 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 956 AA; 104201 MW; AE9B136DF0F5E58 CRC64;

Query Match 40.2%; Score 47; DB 1; Length 956;
Best Local Similarity 45.5%; Pred. No. 18;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QVLEIGRTVCVLSNLRGTR 22
DB 113 QQAGLADGRTHVTLRLRGPSR 134

RESULT 10
YS59_ENTFA STANDARD; PRT; 58 AA.
ID YS59_ENTFA
AC 0830C9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable tautomerase EF2859 (EC 5.3.2.-).
GN EF2859.
OS Enterococcus faecalis (Streptococcus faecalis).
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
OX NCBI_TaxID=1351;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=V583 / ATCC 700802;
RX MEDLINE=22550857; PubMed=12663927;
RA Paulsen I.T., Banerjee L., Myers G.S.A., Nelson K.E., Seshadri R.,
RA Read T.D., Fouts D.E., Eisen J.A., Gill S.R., Heidelberg J.F.,
RA Tettelin H., Dodson R.J., Umayam L., Brinkac L., Beanan R.,
RA Daugherty S., DeBoy R.T., Durkin S., Kolonay J., Madupu R., Nelson W.,
RA Vamathevan J., Tran B., Upton J., Hansen T., Shetty J., Khouri H.,
RA Uterback T., Raddue D., Ketchum K.A., Dougherty B.A., Fraser C.M.;
RT "Role of mobile DNA in the evolution of vancomycin-resistant
RT Enterococcus faecalis."
RL Science 299:2071-2074(2003).
CC -1- SIMILARITY: Belongs to the tautomerase family.
CC
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CC
CC -----
CC
CC EMBL; AE016956; AA082551.1; -
CC DR TIGR; EF2859; -
CC DR HAMAP; MF_00718; -; 1.
CC DR InterPro; IPR004370; Taut.
CC DR Pfam; PF01361; Tautomerase; 1.
CC DR ProDom; PD404143; Taut; 1.
CC DR Isoformer; Complete proteome.
CC FT INT MET 0
CC FT ACT SITE 1
CC FT SEQUENCE 58 AA; 6589 MW; FA819A0C5D93CE4E CRC64;

Query Match 39.3%; Score 46; DB 1; Length 58;
Best Local Similarity 60.0%; Pred. No. 1.2;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 VELEIGRTVCVLSNL 17
DB 5 VELEIGRTVEQLTNM 19

RESULT 11
RS28_KLUVA

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ID RS28_KLUVA STANDARD; PRT; 67 AA.
AC P33285;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 40S ribosomal protein S28 (S33).
GN RPS28.
OS Kluyveromyces fragilis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93127729; PubMed=1481571;
RA Hoekstra R., Ferreira P.M., Bootsman T.C., Mager W.H., Planta R.J.;
RT "Structure and expression of the ABF1-regulated ribosomal protein S33
RT gene in Kluyveromyces."
RL Yeast 8:949-959(1992).
CC -1- SIMILARITY: Belongs to the S28E family of ribosomal proteins.
CC
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CC
CC -----
CC
CC EMBL; X69582; CAA49296.1; -
CC DR PIR; S30005; S30005.
CC DR InterPro; IPR000289; Ribosomal_S28e.
CC DR Pfam; PF01200; Ribosomal_S28e; 1.
CC DR ProDom; PD005541; Ribosomal_S28e; 1.
CC DR PROSITE; PS00961; RIBOSOMAL_S28E; 1.
CC KM Ribosomal protein.
SQ SEQUENCE 67 AA; 7536 MW; E5F148312B08A131 CRC64;

Query Match 39.3%; Score 46; DB 1; Length 67;
Best Local Similarity 42.9%; Pred. No. 1.4;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVELEIGRTVCVLSNLRGTR 22
DB 29 RVELEIGRTVIVNVKGPVR 49

RESULT 12
RS28_KLUVA STANDARD; PRT; 67 AA.
ID RS28_KLUVA
AC P33286;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 40S ribosomal protein S28 (S33).
GN RPS28.
OS Kluyveromyces fragilis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=4911;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=CBS 6556;
RX MEDLINE=93127729; PubMed=1481571;
RA Hoekstra R., Ferreira P.M., Bootsman T.C., Mager W.H., Planta R.J.;
RT "Structure and expression of the ABF1-regulated ribosomal protein S33
RT gene in Kluyveromyces."
RL Yeast 8:949-959(1992).
CC -1- SIMILARITY: Belongs to the S28E family of ribosomal proteins.
CC
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CC -----
DR EMBL; X69583; CAA94297.1; -.
DR PIR; S30006; S30006.
DR InterPro; IPR000289; Ribosomal_S28e.
DR Pfam; PF01200; Ribosomal_S28e; 1.
DR ProDom; PD005541; Ribosomal_S28e; 1.
DR PROSITE; PS00961; RIBOSOMAL_S28E; 1.
DR Ribosomal protein.
KW SEQUENCE 67 AA; 7522 MW; E1E55835F18A131 CRC64;
Oy
Db 2 RVEILEGRTECVLSLNGRTR 22
||| ||| :| :| :|
29 RVEFLEDTRTTRVNVKGPVR 49

RESULT 13
C128_MYCTU STANDARD; PRT; 489 AA.
AC Q59572;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Putative cytochrome P450 128 (EC 1.14.--.-).
GN CYP128 OR RV2268C OR MT2330 OR MTCY339.42 OR MB2291C.
OS Mycobacterium tuberculosis.
OS Mycobacterium bovis.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OK NCBI_TaxID=1773, 1765;
[1]
RN SEQUENCE FROM N.A.
RP SPECIES=M.tuberculosis; STRAIN=H37RV;
RC MEDLINE=96295987; PubMed=9634230;
RX Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eigmeier K., Gae S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Pettwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagers K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544 (1998).
[2]
RN SEQUENCE FROM N.A.
RP SPECIES=M.tuberculosis; STRAIN=CDC 1551 / Oshkosh;
RC MEDLINE=22206494; PubMed=1218036;
RX Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,
RA Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and
RT laboratory strains."
RL J. Bacteriol. 184:5479-5490 (2002).
[3]
RN SEQUENCE FROM N.A.
RP SPECIES=M.bovis; STRAIN=AF2122/97;
RC MEDLINE=22709107; PubMed=12788972;
RX Garnier T., Eigmeier K., Camus J.-C., Medina N., Mansoor H.,
RA Pryor M., Duthoy S., Grondin S., Lacroix C., Monsenpe C., Simon S.,
RA Parthill J., Barrall B.G., Cole S.T., Gordon S.V., Hewinson R.G.;
RT "The complete genome sequence of Mycobacterium bovis."
RL Proc. Natl. Acad. Sci. U.S.A. 100:7877-7882 (2003).

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CC -I SUBCELLULAR LOCATION: Integral membrane protein.
CC -I SIMILARITY: Belongs to the cytochrome P450 family.
-----
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CC -----
DR EMBL: Z77163; CAB00967.1; -.
DR EMBL: AE007076; AAA66612.1; -.
DR EMBL: BX248342; CAD97152.1; -.
DR PIR: H70729; H70729.
DR HSSP: 000441; 10XA.
DR TIGR: MT2330; -.
DR TubercuList: RV2268c; -.
DR InterPro: IPR01128; Cytochrome_P450.
DR Pfam: PF00067; P450; 1.
DR PRINTS: PR00385; P450.
DR PROSITE: PS00086; CYTOCHROME_P450; 1.
KW Hypothetical protein: Oxidoreductase; Monooxygenase; Heme;
KW Transmembrane; Complete proteome.
FT TRANSMEM 207 227 POTENTIAL.
FT TRANSMEM 256 276 POTENTIAL.
FT TRANSMEM 315 335 POTENTIAL.
FT TRANSMEM 383 403 POTENTIAL.
FT METAL 435 435 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 489 AA; 53313 MW; 633F233CEFD0AD7A CRC64;

Query Match 39.3%; Score 46; DB 1; Length 489;
Best Local Similarity 47.6%; Pred. No. 13;
Matches 10; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 RVEIEGRTCEVLNLRGTR 22
   ||::|||::|::|::|
DB 458 RIEVEPEPTWTNANLRGLTR 478

RESULT 14
AMS2_SCHPO STANDARD; PRT; 697 AA.
ID AMS2_SCHPO
AC Q9UTJ4; Q9P721;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE CENP-A multicopy suppressor protein 2.
GN AMS2 OR SPC290.04 OR SPC4F11.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_taxid=4896;
OK [1]
RN SEQUENCE FROM N.A.
RP STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gentile S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T.,
RA Woodward J., Volkmar G., Aert R., Roben J., Grympospre B.,
RA Welter I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabell C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,

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RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,
RA Beer P., Zimmermann W., Medler H., Wambutt R., Punnett B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Gilbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Roche M., Galliard C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forstburg S.L.,
RA Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrell B.G., Nure P.;
RA "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
RN
RP [2]
RP FUNCTION, SUBUNIT, AND SUBCELLULAR LOCATION.
RX MEDLINE=22423783; PubMed=12535531;
RA Chen E.S., Saich S., Yanagida M., Takahashi K.;
RT "A cell cycle-regulated GATA factor promotes centromeric localization
RT of CENP-A in fission yeast.";
RL Mol. Cell 11:175-187(2003).
CC -1- FUNCTION: Required for proper chromosome segregation via
CC regulation of CENP-A localization to the centromere.
CC -1- SUBUNIT: Interacts with CENP-A.
CC -1- SUBCELLULAR LOCATION: Nuclear; centromeric.
CC -1- SIMILARITY: Contains 1 GATA-type zinc finger.
CC -----
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CC -----
DR EMBL: AL035260; CAB61504.1; -.
DR EMBL: AL117389; CAB55767.2; -.
DR GeneDB: SPombe; SPCC290.04; -.
DR GO: GO:0005694; C:chromosome; ISS.
DR GO: GO:0005694; C:nucleoplasm; ISS.
DR GO: GO:0007049; P:cell cycle; ISS.
DR InterPro: IPR000679; Znf_GATA.
DR SMART: SM00401; Znf_GATA.1.
DR PROSITE: PS00344; GATA_ZN_FINGER_1; FALSE_NEG.
DR PROSITE: PS50114; GATA_ZN_FINGER_2; 1.
KW Transcription regulation; Nuclear protein; Centromere; DNA-binding;
KW Zinc-finger.
KW ZN_FINGER
SQ SEQUENCE 351 378 GATA-TYPE (ATYPICAL).
Query Match 39.3%; Score 46; DB 1; Length 697;
Best Local Similarity 40.9%; Pred. No. 19;
Matches 9; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
QY 1 ORVEILGRTCEVLSNLRGTR 22
DB 312 EQVRIARGRIKKFTNVGRKR 333

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RESULT 15
YL54_CABEL
ID_YL54_CABEL STANDARD; PRT; 1609 AA.
AC P34434;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein F44E2.4 in chromosome III.
GN F44E2.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peioderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=94150718; PubMed=7906398;

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RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rikken L., Roopra A., Saunders D., Showkeen R.,
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,
RA Watson J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA Wohldman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans.";
RL Nature 368:32-38(1994).
CC -1- SIMILARITY: TO HUMAN KIAA0152.
CC -----
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CC -----
DR EMBL: L23646; AAA28040.1; -.
DR PIR: S44821; S44821.
DR HSSP: P01130; 1AUV.
DR WormPep: F44E2.4; CE00182.
DR Pfam: PF00057; 1d1_recept_a; 1.
DR SMART: SM00192; LDBA; 1.
KW Hypothetical protein.
SQ SEQUENCE 1609 AA; 175966 MW; 4AB845E2AD2207CB CRC64;

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Query Match 39.3%; Score 46; DB 1; Length 1609;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 5 ILGRTCEVLSN 16
DB 877 LLEGRTSCVVS 888
Search completed: May 6, 2004, 12:45:26
Job time : 12 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:44:02 ; Search time 21 Seconds
(without alignments)
105.353 Million cell updates/sec

Title: US-10-612-885A-1
Perfect score: 117
Sequence: 1 QRVLEIGRTECVLSNLRGRTRY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	100.0	508	1 ZUHUR	erythropoietin rec
2	109	93.2	265	2 S14081	erythropoietin rec
3	109	93.2	507	1 A32385	erythropoietin rec
4	109	93.2	507	1 A46713	erythropoietin rec
5	47	40.2	956	2 A57121	thrombospondin 3 p
6	46	39.3	67	2 S30006	ribosomal protein
7	46	39.3	67	2 S30005	ribosomal protein
8	46	39.3	288	2 T30648	probable DNA-bindi
9	46	39.3	489	1 H70729	cytochrome P450 RV
10	46	39.3	710	2 T41352	probable transcrip
11	45	39.3	1609	2 S44821	F44E2.4 protein -
12	45	38.9	607	1 S42639	ATP-dependent RNA
13	45	38.5	316	2 D83406	probable transmem
14	45	38.5	512	1 D70506	hypothetical prote
15	45	38.5	1036	2 S22383	axomin 1 precursor
16	44.5	38.0	810	2 T44430	protein PV100 [imp
17	44	37.6	47	2 AB0673	30S ribosomal prot
18	44	37.6	195	2 A51823	hypothetical prote
19	43	36.8	84	2 C97995	degenerate transp
20	43	36.8	20	2 A87649	hypothetical prote
21	43	36.8	418	2 C95184	IS1167, transposas
22	43	36.8	418	2 P95096	IS1167, transposas
23	43	36.8	654	2 S67870	hypothetical prote
24	43	36.8	931	2 S66574	transferrin-bindin
25	43	36.8	956	1 A46016	thrombospondin 3 -
26	43	36.8	1437	2 T31053	probable protein-t
27	42.5	36.3	228	2 H71251	hypothetical prote
28	42.5	36.3	1894	2 C54689	protein-tyrosine-p
29	42.5	36.3	1912	2 A56178	protein-tyrosine-p

30	42	35.9	67	1 R3BY33	ribosomal protein
31	42	35.9	67	2 S51401	ribosomal protein
32	42	35.9	231	2 T49830	hypothetical prote
33	42	35.9	255	2 A97877	transposase (orf2)
34	42	35.9	260	2 C98084	degenerate transp
35	42	35.9	283	2 S75226	esterase SL1916 -
36	42	35.9	322	2 D89785	hypothetical prote
37	42	35.9	365	2 J00198	aspartate-semialde
38	42	35.9	418	2 A95168	IS1167, transposas
39	42	35.9	418	2 B95197	IS1167, transposas
40	42	35.9	418	2 E95146	IS1167, transposas
41	42	35.9	418	2 H95208	IS1167, transposas
42	42	35.9	482	2 T46944	thiamin biosynthes
43	42	35.9	482	2 A10554	thiamin biosynthes
44	42	35.9	514	2 T29652	inward rectifier p
45	42	35.9	562	2 E70399	hydrogenase regula

ALIGNMENTS

RESULT 1

ZUHUR
erythropoietin receptor precursor - human
C:Species: Homo sapiens (man)
C>Date: 12-Feb-1993 #sequence, revision 05-Apr-1995 #text change 22-Jun-1999
C:Accession: A43799; A60160; A49824; A53958; A55280; J52563
R:Jones, S.S.; D'Andrea, A.D.; Haines, L.L.; Wong, G.G.
Blood 76, 31-35, 1990
A:Title: Human erythropoietin receptor: cloning, expression, and biologic characterization
A:Accession: A43799; MUID:90304340; PMID:2163696
A:Molecule type: mRNA
A:Residues: 1-508 <JON>
A:Cross-references: GB:M60459; NID:G182244; PIDN:AAAS2403.1; PID:G182245
R:Winkelmann, J.C.; Penny, L.A.; Deaven, L.L.; Forget, B.G.; Jenkins, R.B.
Blood 76, 24-30, 1990
A:Title: The gene for the human erythropoietin receptor: analysis of the coding sequence
A:Reference number: A60160; MUID:90304334; PMID:2163695
A:Accession: A60160
A:Status: not compared with conceptual translation
A:Molecule type: mRNA; DNA
A:Residues: 1-101, 'R', 103-188, 'RP', 191-243, 'E', 245-508 <WIN>
R:Noguchi, C.T.; Bae, K.S.; Chin, K.; Wada, Y.; Schechter, A.N.; Hankins, W.D.
Blood 76, 2548-2556, 1991
A:Title: Cloning of the human erythropoietin receptor gene.
A:Reference number: A49824; MUID:92399733; PMID:1668606
A:Accession: A49824
A:Molecule type: DNA
A:Residues: 1-508 <NOG>
A:Cross-references: GB:S45332; NID:G255496; PIDN:AA823771.1; PID:G255497
A:Experimental source: Placenta
A:Note: sequence extracted from NCBI backbone (NCBI:113293, NCBI:113294)
R:Ehrenman, K.; St. John, T.
Exp. Hematol. 19, 973-977, 1991
A:Title: The erythropoietin receptor gene: cloning and identification of multiple trans
A:Reference number: A53958; MUID:91372359; PMID:1654273
A:Accession: A53958
A:Molecule type: mRNA
A:Residues: 1-508 <EHR>
R:Penny, L.A.; Forget, B.G.
Genomics 11, 974-980, 1991
A:Title: Genomic organization of the human erythropoietin receptor gene.
A:Reference number: A55280; MUID:92147143; PMID:1664413
A:Accession: A55280
A:Molecule type: DNA
A:Residues: 1-17,381-387, 'LPEQOQDA', 391-395,504-508 <PEN>
A:Note: sequence modified after extraction from NCBI backbone
A:Note: the authors translated the codon GAT for residue 31 as B
R:Mauche, L.; Tournamille, C.; Hatlab, C.; Boffa, G.; Cartton, J.P.; Chretien, S.
Blood 76, 2557-2563, 1991
A:Title: Cloning of the gene encoding the human erythropoietin receptor.

A/Reference number: I52563; MUID:92399734; PMID:1668607
A/Accession: I52563
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-96 <RES>
A/Cross-references: GB:M76595; NID:g182147; PIDN:AAA52393.1; PID:g553281
C/Genetic:
A/Gene: GDB:EPOR
A/Cross-references: GDB:125242; OMIM:133171
A/Map position: 19p13.3-19p13.2
A/Intons: 39/1; 84/2; 143/1; 195/3; 247/1; 276/2; 305/3
C/Superfamily: erythropoietin receptor; cytokine receptor homology
C/Keywords: alternative splicing; cytokine receptor; glycoprotein;
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-508/Product: erythropoietin receptor #status predicted <MAT>
F:52-250/Domain: extracellular #status predicted <EXT>
F:52-239/Domain: cytokine receptor homology <CRS>
F:233-237/Region: WSXWS motif
F:251-272/Domain: transmembrane #status predicted <TM>
F:273-508/Domain: intracellular #status predicted <INT>
F:52-62,91-107/Disulfide bonds: #status predicted
F:76/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 100.0%; Score 117; DB 1; Length 508;
Best Local Similarity 100.0%; Pred. No. 2.6e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ORVEILGRTCEVLSNLRGTRY 23
Db 194 QRAVELEGRTECVLSNLRGTRY 216

RESULT 2
S14081
erythropoietin receptor - mouse
C/Species: Mus musculus (house mouse)
C/Date: 18-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C/Accession: S14081; I49653
R/Kuramochi, S.; Ikawa, Y.; Todokoro, K.
J. Mol. Biol. 216, 567-575, 1990
A/Title: Characterization of murine erythropoietin receptor genes.
A/Reference number: S13249; MUID:91080149; PMID:2175360
A/Accession: S14081
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-265 <KUR>
R/Lecombe, C.; Chretien, S.; Lemarchandel, V.; Mayeux, P.; Romeo, P.
J. Biol. Chem. 266, 6952-6956, 1991
A/Title: Spleen focus-forming virus long terminal repeat insertional activation of the m
A/Reference number: I49653; MUID:91201346; PMID:1849897
A/Accession: I49653
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-24 <RES>
A/Cross-references: GB:M62360; NID:g193199; PIDN:AAA37582.1; PID:g193200
C/Superfamily: erythropoietin receptor; cytokine receptor homology
C/Keywords: cytokine receptor; transmembrane protein
F:52-238/Domain: cytokine receptor homology <CRS>

Query Match 93.2%; Score 109; DB 2; Length 265;
Best Local Similarity 91.3%; Pred. No. 2.3e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ORVEILGRTCEVLSNLRGTRY 23
Db 193 QRAVELEGRTECVLSNLRGTRY 215

RESULT 3
A32385
erythropoietin receptor precursor, membrane-bound form - mouse
C/Species: Mus musculus (house mouse)
C/Date: 28-Sep-1990 #sequence_revision 05-Apr-1995 #text_change 22-Jun-1999

C/Accession: A41686; A32385; S13249
R/Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.
Mol. Cell. Biol. 11, 5527-5533, 1991
A/Title: Unregulated expression of the erythropoietin receptor gene caused by insertion
A/Reference number: A41686; MUID:92017832; PMID:1656233
A/Accession: A41686

A/Molecule type: mRNA
A/Residues: 1-507 <HIN>
A/Cross-references: GB:S59388; NID:g237036; PIDN:AAB20029.1; PID:g237037
A/Experimental source: murine erythroleukemia (MEL) cell line F5-5
R/D'Andrea, A.D.; Lodish, H.F.; Wong, G.C.
Cell 57, 277-285, 1989

A/Title: Expression cloning of the murine erythropoietin receptor.
A/Reference number: A32385; MUID:89195238; PMID:2519263
A/Accession: A32385

A/Molecule type: mRNA
A/Residues: 1-507 <DNA>
A/Cross-references: GB:U04843; NID:g193090; PIDN:AAA37571.1; PID:g309219
A/Experimental source: murine erythroleukemia (MEL) cells, subclone 745
R/Kuramochi, S.; Ikawa, Y.; Todokoro, K.
J. Mol. Biol. 216, 567-575, 1990

A/Title: Characterization of murine erythropoietin receptor genes.
A/Reference number: S13249; MUID:91080149; PMID:2175360
A/Accession: S13249

A/Molecule type: DNA; mRNA
A/Residues: 1-507 <KUR>
A/Cross-references: EMBL:X53081; NID:g50861; PIDN:CAA37248.1; PID:g50862
A/Experimental source: murine erythroleukemia K-1 cells

C/Genetic:
A/Intons: 39/1; 83/2; 142/1; 194/3; 246/1; 276/2; 304/3
C/Superfamily: erythropoietin receptor; cytokine receptor homology
C/Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-507/Product: erythropoietin receptor #status predicted <MAT>
F:52-249/Domain: extracellular #status predicted <EXT>

F:52-238/Domain: cytokine receptor homology <CRS>
F:250-271/Domain: transmembrane #status predicted <TM>
F:272-507/Domain: intracellular #status predicted <INT>
F:52-62,90-106/Disulfide bonds: #status predicted
F:75/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 93.2%; Score 109; DB 1; Length 507;
Best Local Similarity 91.3%; Pred. No. 4.6e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 ORVEILGRTCEVLSNLRGTRY 23
Db 193 QRAVELEGRTECVLSNLRGTRY 215

RESULT 4
A46713
erythropoietin receptor precursor - rat
C/Species: Rattus norvegicus (Norway Rat)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C/Accession: A46713
R/Masuda, S.; Nago, M.; Takahata, K.; Konishi, Y.; Gallyas Jr., F.; Tabira, T.; Sasaki, J.
J. Biol. Chem. 266, 11208-11216, 1993
A/Title: Functional erythropoietin receptor of the cells with neural characteristics. Com
A/Reference number: A46713; MUID:9326574; PMID:7664373
A/Accession: A46713
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-507 <MAS>
A/Cross-references: GB:D13566; NID:g286209; PIDN:BA02761.1; PID:g286210
A/Experimental source: PC12 and erythroid cells
A/Note: sequence extracted from NCBI backbone (NCBIN:132811, NCBI:P:132813)
C/Superfamily: erythropoietin receptor; cytokine receptor homology
C/Keywords: cytokine receptor; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-507/Product: erythropoietin receptor #status predicted <MAT>
F:25-249/Domain: extracellular #status predicted <EXT>
F:52-238/Domain: cytokine receptor homology <CRS>

F:250-271/Domain: transmembrane #status predicted <TM>
F:272-507/Domain: intracellular #status predicted <INT>
F:75/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 93.2%; Score 109; DB 1; Length 507;
Best Local Similarity 91.3%; Pred. No. 4.6e-09;
Matches 21; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGRTY 23
DB 193 QRVLEGRTECVLSNLRGRTY 215

RESULT 5

A57121
thrombospondin 3 precursor - human
C/Species: Homo sapiens (man)
C/Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 21-Jan-2000
C/Accession: A57121; T08830
R/Adolph, K.W.; Long, G.L.; Winfield, S.; Glines, E.I.; Bornstein, P.
Genomics 27, 329-336, 1995
A/Title: Structure and organization of the human thrombospondin 3 gene (THBS3).
A/Reference number: A57121; MUID:96044440; PMID:7558000
A/Accession: A57121
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-956 <ADO>
A/Cross-references: GB:L38969, NID:g886298, PIDN:AAC41762.1, PID:g886299, GB:L38970
R/Winfield, S.L.; Tayebi, N.; Martin, B.M.; Glines, E.I.; Sidransky, E.
Genome Res. 7, 1020-1026, 1997
A/Title: Identification of three additional genes contiguous to the glucocerebrosidase 1
A/Reference number: Z16482; MUID:97474796; PMID:9331372
A/Accession: T08830
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-736 <WIN>
A/Cross-references: EMBL:AF023268; NID:g2564910; PIDN:AAC51818.1; PID:g2564912
C/Genetics:
A/Gene: GDB:THBS3
A/Cross-references: GDB:409953; OMIM:188062
A/Map position: 1q21-1q23
A/Intons: 27/1; 96/1; 181/3; 216/1; 225/1; 256/1; 270/1; 319/3; 366/3; 392/3; 443/3; 48
C/Function: mediates cell-to-matrix and cell-to-cell interactions
A/Description: thrombospondin 3; EGF homology
F:374-412/Domain: EGF homology <EGF>

Query Match 40.2%; Score 47; DB 2; Length 956;
Best Local Similarity 45.5%; Pred. No. 41;
Matches 10; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 QRVLEGRTECVLSNLRGRTY 22
DB 113 QQAGLADGRHTTVLLRLRGPFR 134

RESULT 6

S30006
ribosomal protein S28.e - Yeast (Kluyveromyces marxianus)
N/Alternate names: ribosomal protein Y533
C/Species: Kluyveromyces marxianus
C/Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 07-May-1999
C/Accession: S30006
R/Hoekstra, R.; Ferreira, P.M.; Bootsman, T.C.; Mager, W.H.; Planta, R.J.
Yeast 8, 949-959, 1992
A/Title: Structure and expression of the ABP1-regulated ribosomal protein S33 gene in Kl
A/Reference number: S30005; MUID:93127729; PMID:1481571
A/Accession: S30006
A/Molecule type: DNA
A/Residues: 1-67 <HOE>
A/Cross-references: GB:S52656
C/Genetics:
A/Gene: S33

C/Superfamily: rat ribosomal protein S28
C/Keywords: protein biosynthesis; ribosome

Query Match 39.3%; Score 46; DB 2; Length 67;
Best Local Similarity 42.9%; Pred. No. 3.7;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVEILEGRTECVLSNLRGRTY 22
DB 29 RVEFLEDTRITIVRNKGPVR 49

RESULT 7

S30005
ribosomal protein S28.e - Yeast (Kluyveromyces marxianus var. lactis)
N/Alternate names: ribosomal protein Y533
C/Species: Kluyveromyces marxianus var. lactis, Candida spherica
C/Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 07-May-1999
C/Accession: S30005
R/Hoekstra, R.; Ferreira, P.M.; Bootsman, T.C.; Mager, W.H.; Planta, R.J.
Yeast 8, 949-959, 1992
A/Title: Structure and expression of the ABP1-regulated ribosomal protein S33 gene in Kl
A/Reference number: S30005; MUID:93127729; PMID:1481571
A/Accession: S30005
A/Molecule type: DNA
A/Residues: 1-67 <HOE>
A/Cross-references: GB:S53420
C/Genetics:
A/Gene: S33
C/Superfamily: rat ribosomal protein S28
C/Keywords: protein biosynthesis; ribosome

Query Match 39.3%; Score 46; DB 2; Length 67;
Best Local Similarity 42.9%; Pred. No. 3.7;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVEILEGRTECVLSNLRGRTY 22
DB 29 RVEFLEDTRITIVRNKGPVR 49

RESULT 8

T30648
probable DNA-binding protein 46L - Moluscum contagiosum virus 1
N/Alternate names: MC046L
C/Species: Moluscum contagiosum virus 1
C/Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 27-Oct-2003
C/Accession: T30648
R/Sankovich, T.G.; Bugert, J.J.; Sisler, J.R.; Koonin, E.V.; Darai, G.; Moss, B.
Science 273, 813-816, 1996
A/Title: Genome sequence of a human tumorigenic poxvirus: Prediction of specific host re
A/Reference number: Z20876; MUID:96325459; PMID:8670425
A/Accession: T30648
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-288 <SPN>
A/Cross-references: EMBL:U60315; NID:g1491943; PIDN:AAC55174.1; PID:g1491989
C/Genetics:
A/Note: MC046L
C/Superfamily: DNA-binding phosphoprotein, vaccinia 13L type
C/Keywords: DNA binding

Query Match 39.3%; Score 46; DB 2; Length 288;
Best Local Similarity 66.7%; Pred. No. 17;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 11 ECVLSNLRGRTY 22
DB 133 ECIYTNLRGRTY 144

RESULT 9

H70729

QY 2 RVEILEGRTECVLSNLGRTRY 23
|| : ||| ||| ||| :
Db 1.95 RVAVLGRAVE--LSPHLGRGW 214

RESULT 14

D70506
hypothetical protein RV2733c - Mycobacterium tuberculosis (strain H37Rv)
C:Species: Mycobacterium tuberculosis
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000
C:Accession: D70506
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; DeLisle, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holtzoyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sibley, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: D70506
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Residues: 1-512 <COL>
A:Molecule type: DNA
A:Cross-references: GB:Z98209; GB:AL123456; NID:g3261838; PIDN:CAB10909.1; PID:g2292967
A:Cross-references source: strain H37Rv
C:Genetics:
A:Gene: RV2733c
A:Superfamily: conserved hypothetical protein b0835

Query Match	38.5%	Score 45;	DB 1;	Length 512;
Best Local Similarity	42.3%;	Pred. No. 44;		
Matches 11;	Conservative 4;	Mismatches 7;	Indels 4;	Gaps 1

```

QY      1 QRVETL---EGRTCEVLNLRGRTR 22
          |||  |||  :  :  :  |||
Db      408 QAVEVLVATGEGRKDVTIARMSGRAR 433

```

RESULT 15

axonin 1 precursor - chicken
 N:Alternate names: neural cell adhesion molecule AxCAM
 C:Species: Gallus gallus (chicken)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 21-Jan-2000
 C:Accession: S52383, S34107, S69332, S22128
 R:Zuellig, R.A.; Rader, C.; Schroeder, A.; Kalousek, M.B.; von Bohlen und Halbach, F.; C
 Bur, J. Biochem. 204, 453-463, 1992
 A:Title: The axonally secreted cell adhesion molecule, axonin-1. Primary structure, immu
 A:Reference number: S22383, MUID:92174898, PMID:1311675
 A:Accession: S22383
 A:Molecule type: mRNA
 A:Residues: 1-1036 <ZuE1>
 A:Cross-references: EMBL:X63101, NID:G62852, PIDN:CAA44815.1, PID:G62853
 A:Accession: S34107
 A:Molecule type: protein
 A:Residues: 29-49;51-80;84-95;100-117;120-128;130-141;143-176;243-254;256-296;303-336;33
 R:Gisler, R.U.; Vogt, L.; Zuellig, R.A.; Rader, C.; Hennehan-Beatty, A.; Wolfer, D.P.; Sto
 Bur, J. Biochem. 227, 617-628, 1995
 A:Title: The gene of chicken axonin-1. Complete structure and analysis of the promoter.
 A:Reference number: S69332, MUID:95172044, PMID:7867620
 A:Accession: S69332
 A:Status: preliminary, nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1002-1036 <GIG>
 A:Cross-references: EMBL:X79607
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
 C:Superfamily: contactin; fibronectin type III repeat homology; immunoglobulin homology
 C:Keywords: cell adhesion
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-1036/Product: axonin 1 #status predicted <MAT>
 F:336-392/Domain: immunoglobulin homology <IMM>

Best Local Similarity 47.1%; Pred. No. 92;
Matches 8; Conservative 2; Mismatches 7; Indels 0; Gaps 0

Search completed: May 6, 2004, 12:47:27
Job time : 22 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:38:56 ; Search time 54 Seconds
(without alignments)
120.344 Million cell updates/sec

Title: US-10-612-885A-1
Perfect score: 117
Sequence: 1 QRVFVLEGRCTVLSNLRGRTRY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues
Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	117	100.0	23	AAV39411	AAV39411 Human ery
2	117	100.0	23	AAU78011	AAU78011 Human ery
3	117	100.0	23	ABP72837	ABP72837 Erythrocy
4	117	100.0	30	AAK98938	AAK98938 Synthetic
5	117	100.0	211	AAK21686	AAK21686 Human mat
6	117	100.0	225	AAK21685	AAK21685 Human mat
7	117	100.0	438	AAV44622	AAV44622 Truncated
8	117	100.0	438	AAV44623	AAV44623 R154C tru
9	117	100.0	458	AAE28671	AAE28671 Human NOV
10	117	100.0	458	AAE28673	AAE28673 Human NOV
11	117	100.0	458	AAE28675	AAE28675 Human NOV
12	117	100.0	488	AAW08349	AAW08349 EPO-recep
13	117	100.0	503	AAH13012	AAH13012 O-tagged
14	117	100.0	508	AAK06512	AAK06512 EPO recep
15	117	100.0	508	AAK47518	AAK47518 Human EPO
16	117	100.0	508	AAK70032	AAK70032 Human ery
17	117	100.0	508	AAK69503	AAK69503 Human ery
18	117	100.0	508	AAH09173	AAH09173 Human ery
19	111	94.9	508	AAE28677	AAE28677 Human NOV
20	109	93.2	265	AAK50326	AAK50326 Mouse sol
21	109	93.2	507	AAK06511	AAK06511 EPO recep
22	109	93.2	507	AAK47517	AAK47517 MEL EPO r
23	109	93.2	507	AAK69502	AAK69502 Mouse ery
24	102	87.2	507	AAK50327	AAK50327 Mouse sol
25	52	44.4	1026	AAU80379	AAU80379 Human BIG

26	52	44.4	1028	2	AAW29667	AAW29667 Homo sapi
27	49	41.9	49	4	AAAB84225	AAAB84225 A tumour
28	49	41.9	49	5	AAE13249	AAE13249 Human tum
29	49	41.9	199	4	ABG13674	ABG13674 Novel hum
30	49	41.9	221	5	ABP65639	ABP65639 Bifidobac
31	49	41.9	286	5	ABP43791	ABP43791 Protein Krl
32	49	41.9	321	2	AAV02136	AAV02136 Protein e
33	49	41.9	341	4	AAAB97378	AAAB97378 Human Krl
34	49	41.9	373	4	AAAB66034	AAAB66034 Human TAN
35	49	41.9	373	6	ABO32694	ABO32694 Secreted
36	49	41.9	413	4	AAAB84220	AAAB84220 A human t
37	49	41.9	413	5	AAE13244	AAE13244 Human tum
38	49	41.9	451	4	AAAB66063	AAAB66063 Murine pr
39	49	41.9	451	6	ABO32717	ABO32717 Secreted
40	49	41.9	456	4	AAAB66033	AAAB66033 Human TAN
41	49	41.9	456	6	ABO32693	ABO32693 Secreted
42	49	41.9	458	5	AAV02135	AAV02135 HTB247 P
43	49	41.9	470	5	ABG76512	ABG76512 DNA encod
44	49	41.9	470	4	AAAB66083	AAAB66083 Murine TA
45	49	41.9	470	6	ABU08371	ABU08371 Amino aci

ALIGNMENTS

RESULT 1
AAV39411
ID AAV39411 standard; peptide; 23 AA.
XX
AC AAV39411;
DT 30-NOV-1999 (first entry)
XX
DE Human erythropoietin receptor-derived activation peptide.
XX
KW Erythropoietin; EPO; receptor; activation; internalisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9942127-A2.
XX
PD 26-AUG-1999.
XX
PF 23-FEB-1999; 99WO-US003910.
XX
PR 24-FEB-1998; 98US-00028938.
XX
PA (RECE-) RECEPTRON INC.
XX
PI Olsson L, Naranda T;
XX
DR WPI; 1999-527422/44.
XX
PT Modulating activity of type-2 cell surface receptors used in treatment
XX of, e.g. Obesity.
XX
PS Claim 8; Page 17; 92pp; English.
XX
XX This sequence represents a peptide derived from the extracellular
XX activation sequence of the human erythropoietin (EPO) receptor.
XX Activation sequences are involved in modulation of receptor responses and
XX are separate from the ligand binding site. Activation of receptor
XX important in two distinct ways: in the modulation of receptor
XX internalisation; and/or in the modulation of activation of the receptor.
XX use of peptides corresponding to the activation sequence of a receptor
XX can retard or inhibit receptor internalisation, thereby increasing or
XX stabilising the steady-state number of active receptors on the cell
XX surface. This has the effect of increasing signalling per unit of ligand.
XX In addition, the receptor is classed as a type 2 cell surface receptor,
XX meaning that such peptides can actually replace the requirement for the
XX ligand, causing ligand-independent activation. This activation is
XX probably brought about by a dimerisation mechanism in which one peptide

CC molecule is bound by two receptors, mimicking the dimerisation and
CC subsequent activation that occurs when two receptors bind one ligand.
CC This peptide could be used to treat disorders involving an inadequate or
CC inappropriate response from its corresponding receptor

XX Sequence 23 AA;

Query Match 100.0%; Score 117; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVEVILEGRTECVLSNLRGRTRY 23
ID 1 QVEVILEGRTECVLSNLRGRTRY 23

Db

RESULT 2
AAU78011
ID AAU78011 standard; peptide; 23 AA.

XX AAU78011;

DT 05-JUN-2002 (first entry)

XX Human erythropoietin receptor activation domain oligopeptide.

XX Erythropoietin receptor; antidiabetic; activation sequence; ligand;
KM receptor internalisation; type 2 diabetes; drug screening; human.

XX Homo sapiens.

XX US6333031-B1.

XX 25-DEC-2001.

XX 24-FEB-1998; 98US-00028937.

XX 08-MAR-1996; 96US-00612999.

XX 22-AUG-1996; 96US-00701382.

XX 23-JAN-1997; 97US-00788820.

XX (RECE-) RECEPTRON INC.

XX Olsson L, Naranda T;

XX WPI; 2002-224899/28.

XX Composition comprising peptides from receptor extracellular domains,
PT useful for e.g. modulating receptor internalization and activation such
PT as increasing insulin activity.

XX Claim 1; Col 11; 48pp; English.

XX This invention corresponds to a novel composition comprising any of 34

XX peptides consisting of activation sequences from the extracellular

XX domains of cell-surface receptors. These peptides were identified by

XX homology searching with a peptide sequence from the MHC class I alpha I

XX domain and correspond to the activation sequences of the associated

XX receptor. Activation sequences are involved in the internalisation of

XX receptors and so these peptides may be used to modulate the

XX internalisation and or activation of these receptors. The peptides of the

XX invention may also be used to increase effect of ligand signalling in

XX type 2 diabetes and can replace the ligand normally required for

XX activation. This is useful when the ligand is a hormone and is difficult

XX to obtain. The peptides may also interact synergistically with the ligand

XX or function as antagonists of receptor signalling. The peptides can also

XX be used in drug screening to identify compounds that modulate receptor

XX internalisation or function as ligand replacements. Use of these peptides

XX can increase the effect of therapeutic hormones (optionally co-

XX administered) by at least 50% and are specific for the receptors from

XX which they derive. The present sequence represents the human

XX Erythropoietin receptor activation sequence oligopeptide of the invention

SQ Sequence 23 AA;

Query Match 100.0%; Score 117; DB 5; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVEVILEGRTECVLSNLRGRTRY 23
ID 1 QVEVILEGRTECVLSNLRGRTRY 23

Db

RESULT 3
ABP72837
ID ABP72837 standard; peptide; 23 AA.

XX ABP72837;

DT 11-AUG-2003 (first entry)

XX Erythropoietin mimetic peptide.

XX Transferrin; neuroprotective; cerebroprotective; vasotropic;
KM antiparkinsonian; nootropic; anti-HIV; antiaesthetic; antiallergic;
KM cytostatic; immunosuppressive; antithrombotic; cardiac;
KM gynaecological; immunostimulant; antianaemic; haemostatic;
KM antiinflammatory; dermatological; antibacterial; virucide; antiparasitic;
KM fungicide; hepatotropic; antirheumatic; antiarthritic; antigout;
KM tranquilizer; vulnery; antidiabetic; nephrotropic; antipyretic;
KM gastrointestinal; gene therapy; transgenic animal; erythropoietin;
KM mimetic; agonist.

XX Synthetic.

XX WO2003020746-A1.

XX 13-MAR-2003.

XX 30-AUG-2002; 2002WO-US027637.

XX 30-AUG-2001; 2001US-0315745P.

XX 30-NOV-2001; 2001US-0334059P.

XX (BIOR-) BIOREXIS PHARM CORP.

XX Prior CP;

XX WPI; 2003-332916/31.

XX New fusion protein, useful in the diagnosis and treatment of diseases or

XX disorders relating to the respiratory, cardiovascular and digestive

XX systems, comprises a transferrin protein fused to a therapeutic protein.

XX Example 9; Page 255; 298pp; English.

XX The present sequence is that of an erythropoietin (EPO) mimetic peptide

XX which has no homology to natural EPO but has similar biological

XX properties in that it activates the EPO receptor acting as an agonist.

XX The EPO mimetic peptide can be included in novel fusion proteins of the

XX invention also including a transferrin (Tf, see ABP72837) moiety

XX engineered to extend the serum half-life or bioavailability. The EPO

XX mimetic peptide can be fused to the N- or C-terminus of Tf, or inserted

XX into, or used to replace part of Tf, such that the Tf acquires EPO

XX activity. Modified Tf fusion proteins of the invention can be used in the

XX diagnosis, prognosis, prevention and/or treatment of diseases and/or

XX disorders of the endocrine, nervous, immune, respiratory, cardiovascular,

XX reproductive and digestive systems, diseases and/or disorders relating to

XX the blood or to cell proliferation, inflammatory conditions and

XX infectious diseases, or to deliver a therapeutic agent to a cell or

XX across the blood-brain barrier

XX Sequence 23 AA;

Query Match 100.0%; Score 117; DB 6; Length 23;

Best Local Similarity 100.0%; Pred. No. 3.6e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRVETLEGRTCVLSNLRGRTRY 23
Db 1 QRVETLEGRTCVLSNLRGRTRY 23

RESULT 4

AAR98938
ID AAR98938 standard; peptide; 30 AA.

XX AAR98938;

XX 28-SEP-1996 (first entry)

XX Synthetic human erythropoietin receptor peptide, SE-8.

XX Monoclonal antibody; erythropoietin receptor; diagnosis; anaemia;

XX erythropoiesis; erythrocyte production; epitope mapping.

XX Synthetic.

XX WO9603438-A1.

XX 08-FEB-1996.

XX 26-JUL-1995; 95WO-US009458.

XX 26-JUL-1994; 94US-00280864.

XX (AMGE-) AMGEN INC.

XX Eliott SG;

XX WPI; 1996-117004/12.

XX Monoclonal antibodies stimulating an erythropoietin receptor - useful in

XX red blood cell levels, e.g. anaemia.

XX Example 6; Page 34; 61pp; English.

XX AAR89960-R89965 and AAR98936-R98939 are overlapping, synthetic human

XX erythropoietin receptor (SHUEPOR) peptides which span residues 1 to 244

XX of the human EPOR. The peptides are used to map the EPOR binding epitope

XX of an EPOR monoclonal antibody which binds to EPORs and stimulates

XX erythropoiesis by stimulating the proliferation and/or differentiation of

XX erythroid progenitor cells to erythrocytes. Pharmaceutical compans.

XX cong. the antibody may be used in the diagnosis and treatment of

XX patients having disorders associated with low red blood cell levels, e.g.

XX anaemia. The antibodies are also useful in methods and kits for detecting

XX EPORs in biological in biological samples

XX Sequence 30 AA;

XX Query Match 100.0%; Score 117; DB 2; Length 30;

XX Best Local Similarity 100.0%; Pred. No. 4.9e-11;

XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1 QRVETLEGRTCVLSNLRGRTRY 23
Db 1 QRVETLEGRTCVLSNLRGRTRY 23

RESULT 5

AAB21686

ID AAB21686 standard; peptide; 211 AA.

XX AAB21686;

XX 21-DEC-2000 (first entry)

DE Human mature erythropoietin receptor EPOR extracellular domain #2.

XX ligand; cell surface receptor; erythropoietin; EPOR; human;

XX protein design automation; FDA.

XX Homo sapiens.

XX WO200047612-A2.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-US003665.

XX 11-FEB-1999; 99US-0120009P.

XX 29-APR-1999; 99US-0131674P.

XX (XENC-) XENCOR INC.

XX Luo P, Dahiya B;

XX WPI; 2000-549135/50.

XX Screening for ligand analogs and agents which modulate ligand-receptor

XX binding, comprises adding a test ligand to a non-naturally occurring cell

XX surface receptor analog.

XX Example 1; Fig 8; 82pp; English.

XX The present invention relates to a method for screening for a ligand

XX analog, comprising adding a candidate ligand to a non-naturally occurring

XX cell surface receptor analog e.g. erythropoietin receptor (EPOR), and

XX determining the binding of the ligand to the analog. The present sequence

XX is a mature human erythropoietin receptor (EPOR) extracellular domain.

XX Protein Design Automation was carried out on the present sequence, so

XX that it may be used in the present invention as a cell surface receptor

XX analog

XX Sequence 211 AA;

XX Query Match 100.0%; Score 117; DB 3; Length 211;

XX Best Local Similarity 100.0%; Pred. No. 4.7e-10;

XX Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX OY 1 QRVETLEGRTCVLSNLRGRTRY 23
Db 161 QRVETLEGRTCVLSNLRGRTRY 163

XX RESULT 6

XX AAB21685

XX ID AAB21685 standard; peptide; 225 AA.

XX AAB21685;

XX 21-DEC-2000 (first entry)

XX Human mature erythropoietin receptor EPOR extracellular domain #1.

XX ligand; cell surface receptor; erythropoietin; EPOR; human.

XX Homo sapiens.

XX WO200047612-A2.

XX 17-AUG-2000.

XX 11-FEB-2000; 2000WO-US003665.

XX 11-FEB-1999; 99US-0120009P.

XX 29-APR-1999; 99US-0131674P.

XX (XENC-) XENCOR INC.

```

PI Luo P, Dahiyat B;
XX
XX WPI; 2000-549135/50.
XX
XX Screening for ligand analogs and agents which modulate ligand-receptor
PT binding, comprises adding a test ligand to a non-naturally occurring cell
PT surface receptor analog.
XX
XX Example 1; Fig 8; 82pp; English.
XX
XX The present invention relates to a method for screening for a ligand
CC analog, comprising adding a candidate ligand to a non-naturally occurring
CC cell surface receptor analog, e.g., erythropoietin receptor (EPOR), and
CC determining the binding of the ligand to the analog. The present sequence
CC is a mature human erythropoietin receptor (EPOR) extracellular domain.
CC This sequence may be used in the present invention as a cell surface
CC receptor analog
XX
XX Sequence 225 AA;
SQ

Query Match          100.0%; Score 117; DB 3; Length 225;
Best Local Similarity 100.0%; Pred. No. 5e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRVETLEGRTCVLSNLRGRTY 23
Db      170 QRVETLEGRTCVLSNLRGRTY 192

RESULT 7
AAV44622
ID AAV44622 standard; protein; 438 AA.
XX
XX AAV44622;
XX
XX 07-APR-2000 (first entry)
XX
XX Truncated human EpOR(t439).
XX
XX Truncated human EpOR; erythropoietin receptor; hypersensitive EpOR(t439);
KM mutant human EpOR; EpOR signalling; cancer; infectious disease; HIV;
KM sickle cell anaemia; cytostatic; antimicrobial; antiviral;
XX immunostimulant; anti-anaemic.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO9967360-A2.
XX
XX 29-DEC-1999.
XX
XX 25-JUN-1999; 99WO-CA000606.
XX
XX 25-JUN-1998; 98CA-02241576.
PR 25-JAN-1999; 99CA-02260332.
XX
XX (HEMO-) HEMOSOL INC.
PA
XX
XX Bell D, Matthews KE, Mueller SG;
PI
XX
XX WPI; 2000-136979/12.
DR
XX P-PSDB; AAZ49634.
XX
XX Serum free defined medium useful for the efficient culture of stem cells
PT used for production of hemoglobin.
XX
XX Example 6; Fig 9; 61pp; English.
XX
XX The present sequence is truncated human EpOR (erythropoietin receptor).
CC Transfection of constitutively active EpOR(t439) by electroporation into
CC a cytokine-dependent cell line supports cell population expansion in the
CC absence of exogenous cytokines. Mutant human EpOR is used in treatment of
CC disorders related to inadequate EpOR signalling. The transfected cells
CC may also used in gene therapy to treat cancer, infectious diseases (e.g.

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CC HIV), sickle cell anaemia, and conditions related to abnormal expression
CC of erythropoietin
XX
XX Sequence 438 AA;
SQ

Query Match          100.0%; Score 117; DB 3; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRVETLEGRTCVLSNLRGRTY 23
Db      194 QRVETLEGRTCVLSNLRGRTY 216

RESULT 8
AAV44623
ID AAV44623 standard; protein; 438 AA.
XX
XX AAV44623;
XX
XX 07-APR-2000 (first entry)
XX
XX R154C truncated human EpOR(t439).
XX
XX Truncated human EpOR; erythropoietin receptor; hypersensitive EpOR(t439);
KM mutant human EpOR; EpOR signalling; cancer; infectious disease; HIV;
KM sickle cell anaemia; cytostatic; antimicrobial; antiviral;
XX immunostimulant; anti-anaemic.
XX
XX Homo sapiens.
XX
XX OS
XX FH Key Location/Qualifiers
XX FT Misc-difference 154
XX PT /note= "Wild type Arg substituted by Cys"
XX
XX PN WO9967360-A2.
XX
XX 29-DEC-1999.
XX
XX 25-JUN-1999; 99WO-CA000606.
XX
XX 25-JUN-1998; 98CA-02241576.
PR 25-JAN-1999; 99CA-02260332.
XX
XX (HEMO-) HEMOSOL INC.
PA
XX
XX Bell D, Matthews KE, Mueller SG;
PI
XX
XX WPI; 2000-136979/12.
DR
XX N-PSDB; AAZ49636.
XX
XX Serum free defined medium useful for the efficient culture of stem cells
PT used for production of hemoglobin.
XX
XX Example 6; Fig 10; 61pp; English.
XX
XX The present sequence is R154C truncated human EpOR (erythropoietin
CC receptor). Transfection of constitutively active EpOR(t439; R154C) by
CC electroporation into a cytokine-dependent cell line supports cell
CC population expansion in the absence of exogenous cytokines. Mutant human
CC EpOR is used in treatment of disorders related to inadequate EpOR
CC signalling. The transfected cells may also used in gene therapy to treat
CC cancer, infectious diseases (e.g. HIV), sickle cell anaemia, and
CC conditions related to abnormal expression of erythropoietin
XX
XX Sequence 438 AA;
SQ

Query Match          100.0%; Score 117; DB 3; Length 438;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRVETLEGRTCVLSNLRGRTY 23

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PR 17-APR-2002; 2002US-0373288P.
 PR 15-MAY-2002; 2002US-0380981P.
 PR 17-MAY-2002; 2002US-0381495P.
 PR 28-MAY-2002; 2002US-0383534P.
 PR 28-MAY-2002; 2002US-0383744P.
 PR 29-MAY-2002; 2002US-0383829P.
 PR 29-MAY-2002; 2002US-0384024P.
 PR 07-AUG-2002; 2002US-0401788P.
 PR 26-AUG-2002; 2002US-0406353P.
 PR 31-OCT-2002; 2002US-00287971.

XX (CURA-) CURAGEN CORP.

PI Alsbrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL,
 PI Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
 PI Ellerman K, Ettenberg S, Gangoli EA, Gerlach VL, Gorman L;
 PI Grose WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;
 PI Lepley DM, Li L, MacDougall JR, Malyaner UM, Mazur A, McQueney K;
 PI Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patuajan M;
 PI Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;
 PI Sultson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twomlow N;
 PI Verneer CAM, Zehrusen BD, Zhong M;

XX WPI; 2003-441555/41.
 DR N-PSDB; ADE28672.

PT New isolated NOX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOX-associated disorders, e.g.
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
 PT asthma, or infections.

XX Claim 1; SEQ ID NO 50; 447bp; English.

CC The invention relates to a novel isolated NOX polypeptide. The
 CC polypeptide of the invention demonstrates, antidiabetic, anorectic,
 CC cardiant, hypotensive, antiarteriosclerotic, virucide, antibacterial,
 CC fungicide, protozoacide, nootropic, neuroprotective, antiparkinsonian,
 CC anticonvulsant, osteopathic, antiarthritic, antiinflammatory,
 CC dermatological, antiaesthetic and antilipemic activities. The
 CC polypeptides, nucleic acid molecules and antibodies may be useful for
 CC treating or diagnosing diseases including metabolic disorders such as
 CC diabetes and obesity, infectious diseases, anorexia, cancer,
 CC cardiovascular diseases including hypertension and atherosclerosis,
 CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's
 CC disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic
 CC disorders, inflammatory skin disorders, asthma and dyslipidaemia.
 CC Furthermore, the nucleic acids and polypeptides may also be used to
 CC identify molecules that modulate or inhibit neurogenesis, cell
 CC differentiation and proliferation, haemopoiesis, wound healing and
 CC angiogenesis, as well as in gene therapy. Finally, the nucleic acids may
 CC be used as hybridisation probes, in chromosome mapping, tissue typing,
 CC preventive medicine and pharmacogenomics. The current sequence is that of
 CC the human NOV protein of the invention.

XX Sequence 458 AA;

Query Match 100.0%; Score 117; DB 7; Length 458;

Best Local Similarity 100.0%; Pred. No. 1.1e-09; Indels 0; Gaps 0;
 Matches 22; Conservative 0; Mismatches 0;

QY 1 QRVETLGRTECVLSNLRGRTRY 23
 Db 194 QRVETLGRTECVLSNLRGRTRY 216

RESULT 11
 ADE28675
 ID ADE28675 standard; protein; 458 AA.

XX ADE28675;

XX 29-JAN-2004 (first entry)

XX

DE Human NOV15c protein - SEQ ID 52.

XX NOX; antidiabetic; anorectic; cardiant; hypotensive;
 XX antiarteriosclerotic; virucide; antibacterial; fungicide; protozoacide;
 XX neurotropic; neuroprotective; antiparkinsonian; anticonvulsant;
 XX osteopathic; antiarthritic; antiinflammatory; dermatological;
 XX anorexia; cancer; cardiovascular; hypertension; atherosclerosis;
 XX neurodegenerative; Alzheimer's disease; Parkinson's; epilepsy; immune;
 XX osteoarthritis; haemopoietic; inflammatory skin; asthma; dyslipidaemia;
 XX neurogenesis; cell differentiation; proliferation; haemopoiesis;
 XX wound healing; angiogenesis; gene therapy; chromosome mapping;
 XX tissue typing; human; NOV.

OS Homo sapiens.

PN WO2003040330-A2.

PD 15-MAY-2003.

XX 05-NOV-2002; 2002WO-US035536.

XX 05-NOV-2001; 2001US-038626P.

PR 05-DEC-2001; 2001US-038600P.

PR 07-DEC-2001; 2001US-038285P.

PR 12-DEC-2001; 2001US-0341346P.

PR 17-DEC-2001; 2001US-0341477P.

PR 20-DEC-2001; 2001US-0342592P.

PR 27-DEC-2001; 2001US-0344297P.

PR 31-DEC-2001; 2001US-0344903P.

PR 17-APR-2002; 2002US-0373288P.

PR 15-MAY-2002; 2002US-0380981P.

PR 17-MAY-2002; 2002US-0381495P.

PR 28-MAY-2002; 2002US-0383534P.

PR 28-MAY-2002; 2002US-0383744P.

PR 29-MAY-2002; 2002US-0383829P.

PR 29-MAY-2002; 2002US-0384024P.

PR 07-AUG-2002; 2002US-0401788P.

PR 26-AUG-2002; 2002US-0406353P.

PR 31-OCT-2002; 2002US-00287971.

(CURA-) CURAGEN CORP.

PI Alsbrook JP, Alvarez E, Anderson DW, Baron M, Boldog FL,
 PI Burgess CE, Casman SJ, Chapoval A, Dhanabal M, Edinger SR, Eisen A;
 PI Ellerman K, Ettenberg S, Gangoli EA, Gerlach VL, Gorman L;
 PI Grose WM, Guo X, Hackett C, Ji W, Kekuda R, Khramtsov NV;
 PI Lepley DM, Li L, MacDougall JR, Malyaner UM, Mazur A, McQueney K;
 PI Mezes PS, Miller CE, Millet I, Mishra VS, Padigaru M, Patuajan M;
 PI Pena CEA, Peyman JA, Rastelli L, Rieger DK, Shenoy SG, Shimkets RA;
 PI Sultson G, Starling G, Spytek KA, Stone DJ, Tchernev VT, Twomlow N;
 PI Verneer CAM, Zehrusen BD, Zhong M;

XX WPI; 2003-441555/41.

DR N-PSDB; ADE28674.

PT New isolated NOX polypeptides and polynucleotides, useful for

PT preventing, diagnosing or treating NOX-associated disorders, e.g.

PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,

PT asthma, or infections.

XX Claim 1; SEQ ID NO 52; 447bp; English.

XX The invention relates to a novel isolated NOX polypeptide. The
 CC polypeptide of the invention demonstrates, antidiabetic, anorectic,
 CC cardiant, hypotensive, antiarteriosclerotic, virucide, antibacterial,
 CC fungicide, protozoacide, nootropic, neuroprotective, antiparkinsonian,
 CC anticonvulsant, osteopathic, antiarthritic, antiinflammatory,
 CC dermatological, antiaesthetic and antilipemic activities. The
 CC polypeptides, nucleic acid molecules and antibodies may be useful for
 CC treating or diagnosing diseases including metabolic disorders such as
 CC diabetes and obesity, infectious diseases, anorexia, cancer,

CC cardiovascular diseases including hypertension and atherosclerosis,
 CC neurodegenerative disorders such as Alzheimer's disease, Parkinson's
 CC disease and epilepsy, immune disorders e.g. osteoarthritis, haemopoietic
 CC disorders, inflammatory skin disorders, asthma and dyslipidaemia.
 CC Furthermore, the nucleic acids and polypeptides may also be used to
 CC identify molecules that modulate or inhibit neurogenesis, cell
 CC differentiation and proliferation, haemopoiesis, wound healing and
 CC angiogenesis, as well as in gene therapy. Finally, the nucleic acids may
 CC be used as hybridisation probes, in chromosome mapping, tissue typing,
 CC preventive medicine and pharmacogenomics. The current sequence is that of
 CC the human NOV protein of the invention.

XX
 SQ Sequence 458 AA;

Query Match 100.0%; Score 117; DB 7; Length 458;
 Best Local Similarity 100.0%; Pred. No. 1.1e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVETLEGRTCVLSNLRGRTRY 23
 DB 194 QRVETLEGRTCVLSNLRGRTRY 216

RESULT 12
 AAW08349
 ID AAW08349 standard; protein; 488 AA.

XX AAW08349;

DT 14-MAR-1997 (first entry)

XX EporFc fusion protein.

XX Receptor agonist; antibody; erythropoietin receptor; Epor; immunogen;
 KM antigen; metallochionein; promoter; IgG1; Fc; anaemia; therapy.

XX Homo; sapiens.

OS Synthetic.

OS Chimeric.

XX Key Location/Qualifiers

FT Domain 1..250

FT /label= Epor-BCD

FT /note= "erythropoietin receptor extracellular domain"

FT /note= "Factor Xa cleavage site"

FT Domain 251..254

FT 255..488

FT /label= Fc

FT /note= "human IgG1 Fc sequence"

XX WO9640231-A1.

PD 19-DEC-1996.

XX 19-DEC-1996.

PF 07-JUN-1996; 96WO-US009613.

PR 07-JUN-1995; 95US-00474673.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Young PR, Erickson-Miller CL;

PI WPI; 1997-051900/05.

XX N-PSDB; AAT48800.

DR N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

XX N-PSDB; AAT48800.

CC fused (via a Factor Xa cleavage sequence) to the Fc portion of human
 CC IgG1. It can be expressed e.g. in transfected Drosophila S2 cells upon
 CC induction with copper sulphate. The cells secrete EporFc as a dimeric
 CC molecule due to the affinity of the Fc moiety for itself. The dimeric
 CC receptor can be used as an immunogen to generate antibodies (monoclonal),
 CC polyclonal, chimeric, humanised) able to act as Ecor agonists for use in
 CC treatment of anaemia

XX
 SQ Sequence 488 AA;

Query Match 100.0%; Score 117; DB 2; Length 488;
 Best Local Similarity 100.0%; Pred. No. 1.2e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVETLEGRTCVLSNLRGRTRY 23
 DB 194 QRVETLEGRTCVLSNLRGRTRY 216

RESULT 13
 AAB13012
 ID AAB13012 standard; protein; 503 AA.

XX AAB13012;

DT 08-DEC-2000 (first entry)

XX Q-tagged erythropoietin (EPO) receptor protein.

XX Site specific label; detection; interaction screening; transglutaminase;
 KM erythropoietin receptor; EPO.

XX Synthetic.

XX WO200043492-A2.

XX 27-JUL-2000.

XX 27-JUL-2000.

XX 27-JUL-2000.

XX 27-JUL-2000.

XX 27-JUL-2000.

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XX 27-JUL-2000.

XX 27-JUL-2000.

XX 27-JUL-2000.

CC fused (via a Factor Xa cleavage sequence) to the Fc portion of human
 CC IgG1. It can be expressed e.g. in transfected Drosophila S2 cells upon
 CC induction with copper sulphate. The cells secrete EporFc as a dimeric
 CC molecule due to the affinity of the Fc moiety for itself. The dimeric
 CC receptor can be used as an immunogen to generate antibodies (monoclonal),
 CC polyclonal, chimeric, humanised) able to act as Ecor agonists for use in
 CC treatment of anaemia

XX
 SQ Sequence 503 AA;

Query Match 100.0%; Score 117; DB 3; Length 503;
 Best Local Similarity 100.0%; Pred. No. 1.3e-09;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVETLEGRTCVLSNLRGRTRY 23
 DB 194 QRVETLEGRTCVLSNLRGRTRY 216

RESULT 13
 AAB13012
 ID AAB13012 standard; protein; 503 AA.

XX AAB13012;

DT 08-DEC-2000 (first entry)

XX Q-tagged erythropoietin (EPO) receptor protein.

XX Site specific label; detection; interaction screening; transglutaminase;
 KM erythropoietin receptor; EPO.

XX Synthetic.

XX WO200043492-A2.

XX 27-JUL-2000.

XX 27-JUL-2000.

XX 27-JUL-2000.

XX 27-JUL-2000.

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XX 27-JUL-2000.

XX 27-JUL-2000.

XX 27-JUL-2000.

XX 27-JUL-2000.

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Db          194 QRVETLGRTECVLSNLRGRTRY 216

RESULT 14
AA06512
ID   AA06512 standard; protein; 508 AA.
XX
AC   AA06512;
XX
DT   25-MAR-2003 (revised)
DT   04-JAN-1991 (first entry)
XX
DE   EPO receptor.
XX
KM   Erythropoietin; Diamond Blackfan anaemia; polycythemia vera.
XX
OS   Homo sapiens.
XX
PN   W09008822-A.
XX
PD   09-AUG-1990.
XX
PF   03-FEB-1989; 89US-00306503.
XX
PR   03-FEB-1989; 89US-00306503.
XX
PA   (GEMV ) GENETICS INST INC.
PA   (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
PI   Dandrea A, Wong G;
XX
DR   WPI; 1990-260931/34.
DR   N-PSDB; AAQ05748.
XX
PT   Erythropoietin receptor and gene - used for developing reagents and
PT   systems to control and study erythropoiesis.
XX
PS   Disclosure; Fig 2; 53pp; English.
XX
CC   The sequence was deduced from DNA obtd. from a clone isolated from a
CC   commercially available human genomic cDNA library in phage Lambda Fix
CC   (Stratagene). The sequence encodes a type I trans-membrane protein with
CC   binding affinity for EPO. The gene and recombinant EPO receptor produced
CC   on expression of the DNA are used to develop reagents and systems to
CC   control and study erythropoiesis. It is believed that the EPO receptor is
CC   dys- functional in individuals with Diamond Blackfan anemia, and may be
CC   hyperactive in polycythemia vera. See also AA06511 (murine EPO
CC   receptor). (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-
CC   MAR-2003 to correct PI field.)
XX
SQ   Sequence 508 AA;

Query Match          100.0%; Score 117; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 QRVETLGRTECVLSNLRGRTRY 23
Db          194 QRVETLGRTECVLSNLRGRTRY 216

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XX          XX Homo sapiens.
OS
XX
XX          Key Location/Qualifiers
FH          Peptide 1..24
FT          /note= "signal peptide"
FT          Protein 25..508
FT          /note= "mature EPO receptor"
FT          Region 251..272
FT          /note= "putative transmembrane domain"
XX
XX          US5278065-A.
XX
XX          11-JAN-1994.
XX
XX          25-MAR-1991; 91US-00678877.
XX
XX          03-FEB-1989; 89US-00306503.
XX
XX          (GEMV ) GENETICS INST INC.
XX          (CHIL-) CHILDRENS MEDICAL CENT.
XX          (WHED ) WHITEHEAD INST BIOMEDICAL RES.
XX
XX          D'andrea A, Wong GG, Jones SS;
XX
XX          WPI; 1994-025409/03.
XX          DR   N-PSDB; AAQ53995.
XX
XX          Recombinant DNA encoding erythropoietin receptor - used to develop prods.
XX          for study, treatment or diagnosis of disorders in which receptor is
XX          dysfunctional.
XX
XX          Disclosure; Fig 9; 24pp; English.
XX
XX          Mouse erythroleukaemia (MEL) cells were used to construct a cDNA library.
XX          The cDNA was used to transfect COS-1 cells and these were screened for
XX          radioliodinated erythropoietin (EPO) binding to isolate cDNA encoding the
XX          EPO receptor. This cDNA was used as a probe to screen a human genomic
XX          cDNA library to obtain DNA encoding the human EPO receptor. The cDNA may
XX          be used to study, treat or diagnose disorders in which the EPO receptor
XX          is dysfunctional. The EPO receptor may also be used to raise antiodied or
XX          for treating hypersensitivity to EPO or who have elevated levels of EPO.
XX          The pord. is pref. used for treating anaemias, primary proliferative
XX          CC polycythemia and secondary polycythemia. See also AA07517. (Updated on
XX          25-MAR-2003 to correct PF field.)
XX
SQ   Sequence 508 AA;

Query Match          100.0%; Score 117; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.3e-09;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 QRVETLGRTECVLSNLRGRTRY 23
Db          194 QRVETLGRTECVLSNLRGRTRY 216

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Search completed: May 6, 2004, 12:45:02
Job time : 55 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:42:22 ; Search time 23 Seconds
(without alignments)
51.626 Million cell updates/sec

Title: US-10-612-885A-1

Perfect score: 117
Sequence: 1 QRVLEIGRTECVLSNLRGRTRY 23

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/1aa/5B-COMB.pep:*
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4: /cgn2_6/ptodata/2/1aa/6B-COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query	Match Length	ID	Description
1	117	100.0	23	US-09-028-937-11	Sequence 11, Appl
2	117	100.0	30	US-08-280-864A-12	Sequence 12, Appl
3	117	100.0	30	US-09-092-291-12	Sequence 12, Appl
4	117	100.0	438	US-09-339-838-5	Sequence 5, Appl
5	117	100.0	438	US-09-339-838-7	Sequence 7, Appl
6	117	100.0	488	US-08-776-511-2	Sequence 2, Appl
7	117	100.0	508	US-08-850-293-5	Sequence 5, Appl
8	49	41.9	321	US-09-039-609-4	Sequence 4, Appl
9	49	41.9	458	US-09-039-609-2	Sequence 2, Appl
10	46	39.3	64	US-09-134-000C-5287	Sequence 5287, Ap
11	46	39.3	67	US-09-732-210-1599	Sequence 1599, Ap
12	46	39.3	67	US-09-732-210-1600	Sequence 1600, Ap
13	45	38.5	372	US-09-252-991A-32067	Sequence 32067, A
14	44	37.6	493	US-09-489-039A-12903	Sequence 12903, A
15	43	36.8	931	US-08-624-655A-2	Sequence 2, Appl
16	42	35.9	67	US-09-732-210-1601	Sequence 1601, Ap
17	42	35.9	252	US-09-252-991A-32222	Sequence 32222, A
18	42	35.9	283	US-08-956-171E-5203	Sequence 5203, Ap
19	42	35.9	363	US-09-134-000C-3764	Sequence 3764, Ap
20	42	35.9	605	US-08-752-307B-8	Sequence 8, Appl
21	42	35.9	605	US-09-707-802-8	Sequence 8, Appl
22	42	35.9	605	US-09-981-326-8	Sequence 8, Appl
23	42	35.9	623	US-09-252-991A-23930	Sequence 23930, A
24	42	35.9	1018	US-08-452-052-2	Sequence 2, Appl
25	42	35.9	1101	US-08-986-485-2	Sequence 2, Appl
26	42	35.9	1611	US-08-804-227C-5	Sequence 5, Appl
27	42	35.9	3729	US-08-804-227C-4	Sequence 4, Appl

28	42	35.9	4472	2	US-08-804-227C-2	Sequence 2, Appl
29	42	35.9	4545	2	US-08-804-227C-14	Sequence 14, Appl
30	41	35.0	50	4	US-09-621-976-6212	Sequence 6212, Ap
31	41	35.0	60	4	US-08-754-477A-14	Sequence 14, Appl
32	41	35.0	60	4	US-08-754-477A-15	Sequence 15, Appl
33	41	35.0	75	3	US-08-928-383B-13	Sequence 13, Appl
34	41	35.0	292	4	US-09-711-164-438	Sequence 438, Ap
35	41	35.0	327	4	US-09-134-001C-3535	Sequence 3535, Ap
36	41	35.0	749	4	US-09-252-991A-17331	Sequence 17331, A
37	41	35.0	835	4	US-09-758-282B-155	Sequence 155, App
38	41	35.0	835	4	US-09-758-282B-243	Sequence 243, App
39	41	35.0	843	4	US-09-489-039A-7545	Sequence 745, Ap
40	41	35.0	865	4	US-09-252-991A-20894	Sequence 20894, A
41	41	35.0	1018	1	US-08-408-093-6	Sequence 6, Appl
42	41	35.0	1018	1	US-08-408-420A-6	Sequence 6, Appl
43	41	35.0	1018	1	US-08-714-901-6	Sequence 6, Appl
44	41	35.0	1018	3	US-08-040-741-6	Sequence 6, Appl
45	41	35.0	1091	3	US-08-986-485-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-09-028-937-11
Sequence 11, Application US/09028937
Patent No. 633031
GENERAL INFORMATION:
APPLICANT: Olsson, Lemnart
APPLICANT: Naranda, Tatjana
TITLE OF INVENTION: Receptor Derived Peptides As Modulators
TITLE OF INVENTION: Of Receptor Activity
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Teest, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028,937
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/788,820
FILING DATE: 23-JAN-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/701,382
FILING DATE: 22-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/612,999
FILING DATE: 08-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Silva, Robin M.
REGISTRATION NUMBER: 38,304
REFERENCE/DOCKET NUMBER: A-63139-3/RFT/RMS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 949-8711
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-09-028-937-11

Query Match 100.0%; Score 117; DB 4; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.3e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTCEVLSNLRGRTRY 23
Db 1 QRVLEIGRTCEVLSNLRGRTRY 23

RESULT 2

US-08-280-864A-12
; Sequence 12, Application US/08280864A
; Patent No. 5885574
; GENERAL INFORMATION:
; APPLICANT: Eliott, Steven G.
; TITLE OF INVENTION: Antibodies Which Activate an
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Denavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/280,864A
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-307
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-280-864A-12

Query Match 100.0%; Score 117; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTCEVLSNLRGRTRY 23
Db 1 QRVLEIGRTCEVLSNLRGRTRY 23

RESULT 3

US-09-092-291-12
; Sequence 12, Application US/09092291
; Patent No. 6319499
; GENERAL INFORMATION:
; APPLICANT: Eliott, Steven G.
; TITLE OF INVENTION: Antibodies Which Activate an
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 91320
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/092,291
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER: US 08/280864
; FILING DATE: 25-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-307A
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-092-291-12

Query Match 100.0%; Score 117; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.8e-12;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTCEVLSNLRGRTRY 23
Db 1 QRVLEIGRTCEVLSNLRGRTRY 23

RESULT 4

US-09-339-838-5
; Sequence 5, Application US/09339838
; Patent No. 6361998
; GENERAL INFORMATION:
; APPLICANT: Bell, David N.
; APPLICANT: Mueller, Susan G.
; APPLICANT: Matthews, Kathryn E.
; TITLE OF INVENTION: The Efficient Culture of Stem Cells for the Production of Hemoglot
; FILE REFERENCE: 6704-83
; CURRENT APPLICATION NUMBER: US/09/339,838
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: CA 2,260,332
; PRIOR FILING DATE: 1999-01-25
; PRIOR APPLICATION NUMBER: CA 2,241,576
; PRIOR FILING DATE: 1998-06-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 5
; LENGTH: 438
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-339-838-5

Query Match 100.0%; Score 117; DB 4; Length 438;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVLEIGRTCEVLSNLRGRTRY 23
Db 194 QRVLEIGRTCEVLSNLRGRTRY 216

RESULT 5

US-09-339-838-7
; Sequence 7, Application US/09339838
; Patent No. 6361998
; GENERAL INFORMATION:
; APPLICANT: Bell, David N.
; APPLICANT: Mueller, Susan G.
; APPLICANT: Matthews, Kathryn E.

;; TITLE OF INVENTION: The Efficient Culture of Stem Cells for the Production of Hemogid
;; FILE REFERENCE: 6704-83
;; CURRENT APPLICATION NUMBER: US/09/339,838
;; CURRENT FILING DATE: 1999-06-25
;; PRIOR APPLICATION NUMBER: CA 2,260,332
;; PRIOR FILING DATE: 1999-01-25
;; PRIOR APPLICATION NUMBER: CA 2,241,576
;; PRIOR FILING DATE: 1998-06-25
;; NUMBER OF SEQ ID NOS: 11
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 7
;; LENGTH: 438
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-339-838-7

Query Match 100.0%; Score 117; DB 4; Length 438;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRVLEIGRTECVLSNLRGRTY 23
Db 194 QRVLEIGRTECVLSNLRGRTY 216

RESULT 6
US-08-776-511-2
;; Sequence 2, Application US/0876511
;; Patent No. 6153190
;; GENERAL INFORMATION:
;; APPLICANT: Young, Peter R.
;; ATTORNEY/AGENT INFORMATION:
;; TITLE OF INVENTION: Method for Obtaining Receptor Agonist
;; TITLE OF INVENTION: Antibodies
;; NUMBER OF SEQUENCES: 13
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: SmithKline Beecham Corporation- Corporate
;; STREET: 709 Swedeland Road
;; CITY: King of Prussia
;; STATE: Pennsylvania
;; COUNTRY: USA
;; ZIP: 19406-2799
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/776,511
;; FILING DATE:
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Jervis, Herbert H.
;; REGISTRATION NUMBER: 31,171
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 610-270-5015
;; TELEFAX: 610-270-5090
;; INFORMATION FOR SEQ ID NO: 2:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 488 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-776-511-2

Query Match 100.0%; Score 117; DB 3; Length 488;
Best Local Similarity 100.0%; Pred. No. 4.9e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRVLEIGRTECVLSNLRGRTY 23
Db 194 QRVLEIGRTECVLSNLRGRTY 216

Db 194 QRVLEIGRTECVLSNLRGRTY 216

RESULT 7
US-08-850-293-5
;; Sequence 5, Application US/08850293
;; Patent No. 5843726
;; GENERAL INFORMATION:
;; APPLICANT: Lee, Jong Y.
;; TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR
;; TITLE OF INVENTION: PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
;; NUMBER OF SEQUENCES: 5
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C., P.A.
;; STREET: 60 South Sixth Street, Suite 3300
;; CITY: Minneapolis
;; STATE: MN
;; COUNTRY: USA
;; ZIP: 55402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/850,293
;; FILING DATE: 05-MAY-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/499,643
;; FILING DATE: 07-JUL-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/106,815
;; FILING DATE: 16-AUG-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ellinger, Mark S.
;; REGISTRATION NUMBER: 34,812
;; REFERENCE/DOCKET NUMBER: 07004/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 612/335-5070
;; TELEFAX: 612/288-9696
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 508 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-850-293-5

Query Match 100.0%; Score 117; DB 2; Length 508;
Best Local Similarity 100.0%; Pred. No. 5.2e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QRVLEIGRTECVLSNLRGRTY 23
Db 194 QRVLEIGRTECVLSNLRGRTY 216

RESULT 8
US-09-039-609-4
;; Sequence 4, Application US/09039609
;; Patent No. 6107473
;; GENERAL INFORMATION:
;; APPLICANT: ALBONE, EARL
;; ATTORNEY/AGENT INFORMATION:
;; NAME: KIRBY, KRISTINE
;; TITLE OF INVENTION: A KRINGLE-RELATED CLONE,
;; TITLE OF INVENTION: HTHE247
;; NUMBER OF SEQUENCES: 4
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Ratner & Prestia
;; STREET: P.O. Box 980
;; CITY: Valley Forge
;; STATE: PA

COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,609
FILING DATE: 16-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,623
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70275
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-039-609-4

Query Match 41.9%; Score 49; DB 3; Length 321;
Best Local Similarity 50.0%; Pred. No. 4.1;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 3 VELEGRTCEVLSNLGRTR 22
DB 226 VEILDGYTHVLARFGRSR 245

RESULT 9
US-09-039-609-2
Sequence 2, Application US/09039609
Patent No. 6107473
GENERAL INFORMATION:
APPLICANT: ALBONE, EARL
APPLICANT: KIRKLY, KRISTINE
TITLE OF INVENTION: A KIRKLY-RELATED CLONE,
TITLE OF INVENTION: HTHB247
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ratner & Prestia
STREET: P.O. Box 980
CITY: Valley Forge
STATE: PA
COUNTRY: USA
ZIP: 19482
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,609
FILING DATE: 16-MAR-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/060,623
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Prestia, Paul F
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GP-70275

TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-039-609-2

Query Match 41.9%; Score 49; DB 3; Length 458;
Best Local Similarity 50.0%; Pred. No. 6.3;
Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 3 VELEGRTCEVLSNLGRTR 22
DB 270 VEILDGYTHVLARFGRSR 289

RESULT 10
US-09-134-000C-5287
Sequence 5287, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stramm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FILE REFERENCE: 032796-032
CURRENT APPLICATION NUMBER: US/09/134,000C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5287
LENGTH: 64
TYPE: PRT
ORGANISM: Enterococcus faecalis
US-09-134-000C-5287

Query Match 39.3%; Score 46; DB 4; Length 64;
Best Local Similarity 60.0%; Pred. No. 1.9;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 VELEGRTCEVLSNL 17
DB 11 VELEGRTCEVLSNL 25

RESULT 11
US-09-732-210-1599
Sequence 1599, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Liang, Jihong
APPLICANT: Miltenk, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 1599
LENGTH: 67

TYPE: PRT
ORGANISM: Kluyveromyces lactis
US-09-732-210-1599

Query Match 39.3%; Score 46; DB 4; Length 67;
Best Local Similarity 42.9%; Pred. No. 2;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVELEGTECVLSNLGRTR 22
DB 29 RVEFLEDTRTIVNVKGPVR 49

RESULT 12
US-09-732-210-1600
Sequence 1600, Application US/09732210
Patent No. 6573361
GENERAL INFORMATION:
APPLICANT: Bunkers, Greg J.
APPLICANT: Mitanck, Cindy A.
APPLICANT: Seale, Jeffrey W.
APPLICANT: Wu, Yonnie S.
TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
FILE REFERENCE: 38-21(15036)B
CURRENT APPLICATION NUMBER: US/09/732,210
CURRENT FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 60/169,513
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: US 60/169,340
PRIOR FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 1753
SEQ ID NO 1600
LENGTH: 67
TYPE: PRT
ORGANISM: Kluyveromyces marxianus
US-09-732-210-1600

Query Match 39.3%; Score 46; DB 4; Length 67;
Best Local Similarity 42.9%; Pred. No. 2;
Matches 9; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 2 RVELEGTECVLSNLGRTR 22
DB 29 RVEFLEDTRTIVNVKGPVR 49

RESULT 13
US-09-252-991A-32067
Sequence 32067, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 32067
LENGTH: 372
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-32067

Query Match 38.5%; Score 45; DB 4; Length 372;
Best Local Similarity 54.5%; Pred. No. 22;
Matches 12; Conservative 2; Mismatches 6; Indels 2; Gaps 1;

QY 2 RVELEGTECVLSNLGRTRY 23
DB 251 RVALAGRV--LSPLHGRGW 270

RESULT 14
US-09-489-039A-12903
Sequence 12903, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 12903
LENGTH: 493
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12903

Query Match 37.6%; Score 44; DB 4; Length 493;
Best Local Similarity 45.0%; Pred. No. 45;
Matches 9; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

QY 4 ELEGTECVLSNLGRTRY 23
DB 111 EALEGTECVVRKRGKHEF 130

RESULT 15
US-08-624-655A-2
Sequence 2, Application US/08624655A
Patent No. 6323005
GENERAL INFORMATION:
APPLICANT: DAHAN, MONTSERRAT
APPLICANT: MEDRANO, ANDRES
APPLICANT: ESPUNA, ENRIC
APPLICANT: QUEROLO, ENRIQUE
TITLE OF INVENTION: TRANSFERRIN-BINDING PROTEIN 1 (Tbp1) GENE OF
TITLE OF INVENTION: Actinobacillus pleuropneumoniae, ITS USE TO PREPARE
PRODUCTS FOR THE UTILIZATION IN VACCINES FOR
TITLE OF INVENTION: PLEURO-PNEUMONIA AND AS DIAGNOSTIC REAGENTS
FILE REFERENCE: P00740
CURRENT APPLICATION NUMBER: US/08/624,655A
CURRENT FILING DATE: 1996-03-22
PRIOR APPLICATION NUMBER: 95 00592
PRIOR FILING DATE: 1995-03-24
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 931
TYPE: PRT
ORGANISM: Actinobacillus pleuropneumoniae
US-08-624-655A-2

Query Match 36.8%; Score 43; DB 4; Length 931;
Best Local Similarity 33.3%; Pred. No. 1.4e+02;
Matches 6; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 6 LEGRTECVLSNLGRTRY 23
DB 581 IAGRADCATSKIKGHNY 598

Search completed: May 6, 2004, 12:46:53
Job time : 23 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: May 6, 2004, 12:45:07 ; Search time 42 Seconds
(Without alignments)
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Title: US-10-612-885A-1

Perfect score: 117

Sequence: 1 QRVETLEGRTECVLSNLRGRTRY 23

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Gapop 10.0 , Gapext 0.5

Searched: 1140673 seqs, 27566755 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	117	100.0	23	9	US-09-991-548-11 Sequence 11, Appl
2	117	100.0	23	16	US-10-231-494-30 Sequence 30, Appl
3	117	100.0	30	15	US-10-364-276-12 Sequence 12, Appl
4	117	100.0	458	12	US-10-287-971-48 Sequence 48, Appl
5	117	100.0	458	12	US-10-287-971-50 Sequence 50, Appl
6	117	100.0	458	12	US-10-287-971-52 Sequence 52, Appl
7	117	100.0	508	9	US-09-016-159-5 Sequence 5, Appl
8	113	96.6	508	12	US-10-287-971-54 Sequence 54, Appl
9	103	88.0	109	15	US-10-316-194-142 Sequence 142, App
10	96	82.1	109	15	US-10-316-194-144 Sequence 144, App
11	93	79.5	109	15	US-10-316-194-35 Sequence 35, Appl
12	86	73.5	109	15	US-10-316-194-43 Sequence 43, Appl
13	52	44.4	1026	10	US-09-947-063-4 Sequence 4, Appl
14	52	44.4	1026	10	US-09-947-063-11 Sequence 11, Appl
15	49	41.9	49	9	US-09-728-912-7 Sequence 7, Appl

16	49	41.9	110	14	US-10-029-386-27439	Sequence 27439, A
17	49	41.9	341	9	US-09-848-288-4	Sequence 4, Appl
18	48	41.9	373	10	US-09-759-130B-376	Sequence 376, App
19	48	41.9	373	13	US-10-042-431-6	Sequence 6, Appl
20	49	41.9	413	9	US-09-728-912-2	Sequence 2, Appl
21	49	41.9	451	10	US-09-759-130B-413	Sequence 413, App
22	49	41.9	451	13	US-10-042-431-43	Sequence 43, Appl
23	49	41.9	456	10	US-09-759-130B-375	Sequence 375, App
24	48	41.9	456	13	US-10-042-431-5	Sequence 5, Appl
25	48	41.9	458	16	US-10-467-042-16	Sequence 16, Appl
26	49	41.9	470	10	US-09-759-130B-439	Sequence 439, App
27	49	41.9	470	13	US-10-042-431-69	Sequence 69, Appl
28	49	41.9	475	10	US-09-759-130B-373	Sequence 373, App
29	49	41.9	475	13	US-10-042-431-3	Sequence 3, Appl
30	48	41.9	492	15	US-10-094-749-2546	Sequence 2546, Ap
31	48	41.0	312	9	US-09-738-626-5282	Sequence 5282, Ap
32	47.5	40.6	419	15	US-10-369-493-9725	Sequence 9725, Ap
33	47	40.2	85	14	US-10-029-386-32900	Sequence 32900, A
34	47	40.2	151	12	US-10-424-599-181458	Sequence 181458,
35	47	40.2	366	12	US-10-424-599-181457	Sequence 181457,
36	46	39.3	494	12	US-10-425-114-50005	Sequence 50005, A
37	46	39.3	941	12	US-10-425-114-72012	Sequence 72012, A
38	45	38.5	686	15	US-10-162-335-46	Sequence 46, Appl
39	45	38.5	686	15	US-10-162-335-48	Sequence 48, Appl
40	45	38.5	686	15	US-10-162-335-50	Sequence 50, Appl
41	45	38.5	686	15	US-10-162-335-52	Sequence 52, Appl
42	45	38.5	961	15	US-10-162-335-42	Sequence 42, Appl
43	44	37.6	87	12	US-10-424-599-196538	Sequence 196538,
44	44	37.6	250	12	US-10-424-599-236053	Sequence 236053,
45	44	37.6	873	12	US-10-425-114-65968	Sequence 65968, A

ALIGNMENTS

```
RESULT 1
US-09-991-548-11
Sequence 11, Application US/09991548
Patent No. US20020160013A1
GENERAL INFORMATION:
APPLICANT: OLSSON, Lennart
APPLICANT: NARANDA, Tactana
TITLE OF INVENTION: RECEPTOR DERIVED PEPTIDES AS MODULATORS
TITLE OF INVENTION: OF RECEPTOR ACTIVITY
FILE REFERENCE: 213542000101
CURRENT APPLICATION NUMBER: US/09/991,548
PRIOR FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 09/028,937
PRIOR FILING DATE: 1998-02-24
PRIOR APPLICATION NUMBER: 08/788,820
PRIOR FILING DATE: 1997-01-23
PRIOR APPLICATION NUMBER: 08/701,382
PRIOR FILING DATE: 1996-08-22
PRIOR APPLICATION NUMBER: 08/612,999
PRIOR FILING DATE: 1996-03-08
NUMBER OF SEQ ID NOS: 44
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 23
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: human erythropoietin receptor
US-09-991-548-11
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Query Match 100.0%; Score 117; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 1,8e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
QY 1 QRVETLEGRTECVLSNLRGRTRY 23
DB 1 QRVETLEGRTECVLSNLRGRTRY 23

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RESULT 2
US-10-231-494-30
; Sequence 30, Application US/10231494
; Publication No. US2004002334A1
; GENERAL INFORMATION:
; APPLICANT: Priot, Christopher P.
; TITLE OF INVENTION: Modified Transferrin Fusion Proteins
; FILE REFERENCE: 54710-5001-US
; CURRENT APPLICATION NUMBER: US/10/231,494
; CURRENT FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: US 60/315,745
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 60/334,059
; PRIOR FILING DATE: 2001-11-30
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 30
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: EPO mimetic
; OTHER INFORMATION: peptide
US-10-231-494-30

Query Match      100.0%; Score 117; DB 16; Length 23;
Best Local Similarity 100.0%; Pred. No.1.8e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRVLEIGRTECVLSNLRGRTRY 23
Db      1 QRVLEIGRTECVLSNLRGRTRY 23

RESULT 3
US-10-364-276-12
; Sequence 12, Application US/10364276
; Publication No. US2003021544A1
; GENERAL INFORMATION:
; APPLICANT: Elliott, Steven G
; TITLE OF INVENTION: Antibodies which Activate an Erythropoietin Receptor
; FILE REFERENCE: 06843-0030-04000
; CURRENT APPLICATION NUMBER: US/10/364,276
; CURRENT FILING DATE: 2003-06-17
; PRIOR APPLICATION NUMBER: 09/092,671
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 08/280,864
; PRIOR FILING DATE: 1994-07-26
; PRIOR APPLICATION NUMBER: 09/640,090
; PRIOR FILING DATE: 2000-08-17
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: peptide
US-10-364-276-12

Query Match      100.0%; Score 117; DB 15; Length 30;
Best Local Similarity 100.0%; Pred. No.2.5e-11;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRVLEIGRTECVLSNLRGRTRY 23
Db      1 QRVLEIGRTECVLSNLRGRTRY 23

RESULT 4
US-10-287-971-48
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; Sequence 48, Application US/10287971
; Publication No. US20040067882A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-480A
; CURRENT APPLICATION NUMBER: US/10/287,971
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/997,425
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 10/035,568
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/338,626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/401,479
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/333,072
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/348,283
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/393,262
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/406,181
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: CuraSeqList Version 0.1
; SEQ ID NO 48
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-971-48

Query Match      100.0%; Score 117; DB 12; Length 458;
Best Local Similarity 100.0%; Pred. No.5.6e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 QRVLEIGRTECVLSNLRGRTRY 23
Db      194 QRVLEIGRTECVLSNLRGRTRY 216

RESULT 5
US-10-287-971-50
; Sequence 50, Application US/10287971
; Publication No. US20040067882A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-480A
; CURRENT APPLICATION NUMBER: US/10/287,971
; CURRENT FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/997,425
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 10/035,568
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/338,626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/401,479
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/333,072
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/348,283
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/393,262
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/406,181
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: CuraSeqList Version 0.1
; SEQ ID NO 50
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-287-971-50

Query Match 100.0%; Score 117; DB 12; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVETLEGRTECVLSNLRGRTRY 23
Db 194 QRVETLEGRTECVLSNLRGRTRY 216

RESULT 6

US-10-287-971-52
; Sequence 52, Application US/10287971
; Publication No. US2004067882A1
; GENERAL INFORMATION:
; APPLICANT: Alcobrook, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-480A
; CURRENT FILING DATE: 2002-11-05
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 09/997,425
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 10/035,568
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/338,626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/401,479
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/333,072
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/348,283
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/393,262
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/406,181
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 397
; SOFTWARE: Curoseqdist version 0.1
; SEQ ID NO 52
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-971-52

Query Match 100.0%; Score 117; DB 12; Length 458;
Best Local Similarity 100.0%; Pred. No. 5.6e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVETLEGRTECVLSNLRGRTRY 23
Db 194 QRVETLEGRTECVLSNLRGRTRY 216

RESULT 7

US-09-016-159-5
; Sequence 5, Application US/09016159
; Patent No. US20020031806A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Jong Y.
; TITLE OF INVENTION: PURIFIED HUMAN ERYTHROPOIETIN RECEPTOR
; TITLE OF INVENTION: PROTEIN FRAGMENT AND ANTIBODIES DERIVED THEREFROM
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C., P.A.
; STREET: 60 South Sixth Street, Suite 3300
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM compatible

OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/016,159
; FILING DATE: 30-JAN-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/876,227
; FILING DATE: 16-JUN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/734,097
; FILING DATE: 21-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460,525
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Ellinger, Mark S.
; REGISTRATION NUMBER: 34,812
; REFERENCE/DOCKET NUMBER: 07004/002003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612/335-5070
; TELEFAX: 612/288-9696
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 508 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-016-159-5

Query Match 100.0%; Score 117; DB 9; Length 508;
Best Local Similarity 100.0%; Pred. No. 6.3e-10;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QRVETLEGRTECVLSNLRGRTRY 23
Db 194 QRVETLEGRTECVLSNLRGRTRY 216

RESULT 8

US-10-287-971-54
; Sequence 54, Application US/10287971
; Publication No. US2004067882A1
; GENERAL INFORMATION:
; APPLICANT: Alcobrook, et al
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-480A
; CURRENT FILING DATE: US/10/287,971
; CURRENT FILING DATE: 2002-11-05
; PRIOR FILING DATE: 2002-11-05
; PRIOR APPLICATION NUMBER: 09/997,425
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: 10/035,568
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/338,626
; PRIOR FILING DATE: 2001-11-05
; PRIOR APPLICATION NUMBER: 60/401,479
; PRIOR FILING DATE: 2002-08-06
; PRIOR APPLICATION NUMBER: 60/333,072
; PRIOR FILING DATE: 2001-11-06
; PRIOR APPLICATION NUMBER: 60/348,283
; PRIOR FILING DATE: 2001-11-09
; PRIOR APPLICATION NUMBER: 60/393,262
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: 60/406,181
; PRIOR FILING DATE: 2002-08-26
; SOFTWARE: Curoseqdist version 0.1
; SEQ ID NO 54
; LENGTH: 508
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-287-971-54

Query Match 96.6%; Score 113; DB 12; Length 508;

Best Local Similarity 82.6%; Pred. No. 8.6e-06;
Matches 19; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 QRVETLGRTECVLSNLRGRTRY 23

Db 46 QRVETLGRTECVLSNLRGRTRY 68

RESULT 13

US-09-947-063-4
; Sequence 4, Application US/09947063
; Publication No. US20030059775A1
; GENERAL INFORMATION:

; APPLICANT: Padigaru et al.

; TITLE OF INVENTION: No. US20030059775A1e1 Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-112

; CURRENT APPLICATION NUMBER: US/09/947,063

; PRIOR FILING DATE: 2001-09-05

; PRIOR APPLICATION NUMBER: 60/229,990

; PRIOR FILING DATE: 2000-09-05

; PRIOR APPLICATION NUMBER: 60/229,988

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 4

; LENGTH: 1026

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-947-063-4

Query Match 44.4%; Score 52; DB 10; Length 1026;

Best Local Similarity 71.4%; Pred. No. 27;

Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 EGRTCEVLSNLRGR 20

Db 292 EGRTCEVLSNLRGR 305

RESULT 14

US-09-947-063-11

; Sequence 11, Application US/09947063

; Publication No. US20030059775A1

; GENERAL INFORMATION:

; APPLICANT: Padigaru et al.

; TITLE OF INVENTION: No. US20030059775A1e1 Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 21402-112

; CURRENT APPLICATION NUMBER: US/09/947,063

; PRIOR FILING DATE: 2001-09-05

; PRIOR APPLICATION NUMBER: 60/229,990

; PRIOR FILING DATE: 2000-09-05

; PRIOR APPLICATION NUMBER: 60/229,988

; NUMBER OF SEQ ID NOS: 30

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 1026

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-947-063-11

Query Match 44.4%; Score 52; DB 10; Length 1026;

Best Local Similarity 71.4%; Pred. No. 27;

Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 7 EGRTCEVLSNLRGR 20

Db 292 EGRTCEVLSNLRGR 305

RESULT 15

US-09-728-912-7

; Sequence 7, Application US/09728912

; Patent No. US20010036643A1

; GENERAL INFORMATION:

; APPLICANT: Holloway, James L.

; TITLE OF INVENTION: Tumor Necrosis Factor-Stimulated Gene

; FILE REFERENCE: 99-94US

; CURRENT APPLICATION NUMBER: US/09/728,912

; PRIOR FILING DATE: 2000-12-01

; PRIOR APPLICATION NUMBER: 60/169,252

; PRIOR FILING DATE: 1999-12-06

; NUMBER OF SEQ ID NOS: 14

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 7

; LENGTH: 49

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-728-912-7

Query Match 41.9%; Score 49; DB 9; Length 49;

Best Local Similarity 50.0%; Pred. No. 2.4;

Matches 10; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 3 VEILGRTECVLSNLRGRTR 22

Db 7 VEILDGYTHRVLARFHGRSR 26

Search completed: May 6, 2004, 12:48:22
Job time : 43 secs

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